



STIC Search Report

Biotech-Chem Library

STIC Database Tracking Number: 109663

**TO: Karen A Lacourciere
Location: CM-1/11D09/11E12
Art Unit: 1635
Monday, December 08, 2003**

Case Serial Number: 09817913

**From: Toby Port
Location: Biotech-Chem Library
CM1-6A04
Phone: 308-3534**

toby.port@uspto.gov

Search Notes

Dear Examiner Lacourciere,

Here are the results of your search.
Please feel free to contact me if you have any questions.

Toby Port

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09/817,913

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: December 5, 2003, 13:02:22 ; Search time 585 Seconds

(without alignments)
11256.261 Million cell updates/sec

Title: US-09-817-913-2

Perfect score: 1611
Sequence: 1 atgtctggggtctctgcccg.....tccctcacgtttcttccccc 1611Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 2888711 seqs, 2045481386 residues

Total number of hits satisfying chosen parameters: 5777422

Minimum DB seq length: 0
Maximum DB seq length: 200000000Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

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GeneBml:
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41: em_hcg_other:*
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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
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| 1 | 1610.6 | 100.0 | 1611 | 6 AX703598 | AX703598 Sequence |
| 2 | 1596.6 | 99.1 | 1611 | 6 AX053101 | AX053101 Sequence |
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| 4 | 1499.6 | 93.1 | 2093 | 9 BC000301 | BC000301 Homo sapi |
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| 6 | 1498 | 93.0 | 2111 | 6 AR012007 | AR012007 Sequence |
| 7 | 1498 | 93.0 | 2111 | 6 E11455 | E11455 cDNA encodi |
| 8 | 1498 | 93.0 | 2111 | 6 I62388 | I62388 Sequence 2 |
| 9 | 1434.2 | 89.0 | 1449 | 12 BR007472 | BR007472 Synthetic |
| 10 | 1240.2 | 77.0 | 1977 | 10 MMHIDE | X98207 M.musculus |
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ALIGNMENTS:

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LOCUS             Sequence 2 from Patent WO03006652.
DEFINITION        AX703598
ACCESSION          AX703598
VERSION            AX703598.1 GI:29538504
KEYWORDS
SOURCE
ORGANISM           Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE          1
AUTHORS            Li, Z., Bonfils, C. and Beestman, J.
TITLE              Inhibition of specific histone deacetylase isoforms
JOURNAL            Patent: WO 0300652-A 2 23-JAN-2003;
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      source                    Location/Qualifiers
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Best Local Similarity 100.0%; Pired. No. 0;
Matches 1611; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 2
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DEFINITION      Sequence 25 from Patent WO0071703.
ACCESSION      AX053101
VERSION      AX053101.1 GI:12227157
KEYWORDS
SOURCE
ORGANISM      Homo sapiens (human)
      Homo sapiens
      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
      Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
1      Macleod A.R., Li Z. and Besterman J.M.
      Inhibition of histone deacetylase
      Patent: WO 0071703-A 25 30-NOV-2000;
      MethyIgene, Inc. (CA)
FEATURES
      source
      1..1611
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      /mol_type="genomic DNA"
      /db_xref="taxon:9606"
BASE COUNT      428 a      385 c      440 g      358 t
ORIGIN

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| Best Local Similarity | 99.4% | Pred. No. 0 | | | |
| Matches 1602 | Conservative | 0 | Mismatches | 9 | Indels |
| | | | | 0 | Gaps |
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| Db | 301 | TGACCAAGTACCAAGGATGACATCAATTAATCTTGCGGCTCATCCGTCAAGATTAACA | 360 | | |
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| Db | 361 | TGTGCGAGTACAGACAGACAGATGACAGATTCAACGTTGGTGAAGGACTGTCCATATTGC | 420 | | |
| QY | 421 | ATGGCCTGTTTGAATTTCTGTCAAGTTGTTCTACGAGGATTCCTGTGGCAAGTCTGTGAAC | 480 | | |
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| Db | 541 | AGTCCGAGGACATCGGGCTTCTGTACGTCATGATGATGATGATGATGATGATGATGATGATG | 600 | | |
| QY | 601 | TAAAGTATCAACAGAGGGTGTCTGTACATTTGACATTTGATTTACACATGATGATGATGATG | 660 | | |
| Db | 601 | TAAAGTATCAACAGAGGGTGTCTGTACATTTGACATTTGATTTACACATGATGATGATGATG | 660 | | |
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| Db | 661 | AAGAGGCTTCTACACACGACCGGGCTATGACTGTGTCTTTTCAATGAATGAGAGT | 720 | | |
| QY | 721 | ACTTCCACAGAACTGGGGGACTTAAGGGATACCGGGGCTGGGAAACAAAGTATATGCTG | 780 | | |
| Db | 721 | ACTTCCACAGAACTGGGGGACTTAAGGGATACCGGGGCTGGGAAACAAAGTATATGCTG | 780 | | |
| QY | 781 | TTAATCAACCCGCTCCGAGACGGGATTTGATGACGATCCTATGAGGCCATTTTCAACGCGG | 840 | | |
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| Db | 961 | GTTGGAATTTGTCAAGACTTTTAACTTTCCTATGCTGAGGACGCGTGGTTTCA | 1020 | | |
| QY | 1021 | CGATTCGTAACGTTGCGCGGATGCTGAGACATATGAGACAGCTGTGGCCTCGATACGAGAA | 1080 | | |

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| Qy | 1141 | ACATCAGTCTCTTCCAAATATGATCTAACCAAGAACAGATGATCTTGGAGAAAGATCAAC | 1200 |
| Db | 1141 | ACATCAGTCTCTTCCAAATATGATCTAACCAAGAACAGATGATCTTGGAGAAAGATCAAC | 1200 |
| Qy | 1201 | AGCAGCTGTTTGGAAACCTTATGAAATGCTGCGGACGCACTCGGGGTCCAAACGAGGCGA | 1260 |
| Db | 1201 | AGCAGCTGTTTGGAAACCTTATGAAATGCTGCGGACGCACTCGGGGTCCAAATGAGGCGA | 1260 |
| Qy | 1261 | TTCTGTAGAGACGCATCCCTGAGAGAGTGGAGTGAAGACGAAGACGACCTTGACAAGC | 1320 |
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| Db | 1501 | AAACCAAGAGAGAGAACCCCAAGAGCCAAAGGGGTCAAGGAGGAGGSTCAAGTTGGGCTGAA | 1560 |
| Qy | 1561 | TGAGACTCTCAGCTCTGGCTTCTGCTGAGATCCCTCAGCTTTCTTTTCCCC | 1611 |
| Db | 1561 | TGAGACTCTCAGCTCTGGCTTCTGCTGAGATCCCTCAGCTTTCTTTTCCCC | 1611 |

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RESULT 3
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LOCUS          HSU50079          1611 bp    mRNA    linear    PRI 16-MAY-1996
DEFINITION    Human histone deacetylase HD1 mRNA, complete cds.
ACCESSION    U50079
VERSION      U50079.1  GI:1277083
KEYWORDS
SOURCE
ORGANISM      Homo sapiens (human)
               Homo sapiens
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               Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE
AUTHORS      Taunton, J., Hassig, C.A. and Schreiber, S.L.
TITLE        A mammalian histone deacetylase related to the yeast
               transcriptional regulator Rpd3p
               Science 272 (5260), 408-411 (1996)
JOURNAL
PUBMED       8602529
REFERENCE    2 (bases 1 to 1611)
AUTHORS      Taunton, J., Hassig, C.A. and Schreiber, S.L.
TITLE        Direct Submission
JOURNAL      Submitted (27-FEB-1996) Jack Taunton, Chemistry, Harvard
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LOCUS      Homo sapiens, similar to histone deacetylase 1, clone MGC:8378
DEFINITION      IMAGE:2820260, mRNA, complete cds.
ACCESSION      BC000301
VERSION      BC000301.1 GI:12653070
KEYWORDS      MGC.
SOURCE      Homo sapiens (human)
ORGANISM      Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE      1 (bases 1 to 2093)
AUTHORS      Strausberg, R.
TITLE      Direct Submission
JOURNAL      Submitted (15-NOV-2000) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,

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REMARK
COMMENT

USA
NIH-MGC Project URL: <http://mgc.nci.nih.gov>
Contact: MGC help desk
Email: cgapbs-remail.nih.gov
Tissue Procurement: DCTD/DRP
CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: National Institutes of Health Intramural
Sequencing Center (NISC),
Gaithersburg, Maryland;
Web site: <http://www.nisc.nih.gov/>
Contact: nisc.mgc@nih.gov
Akher, N., Ayele, K., Beckstrom-Sternberg, S.M., Benjamin, B.,
Bialesley, R.W., Bouffard, G., Breen, K., Brinkley, C., Brooks, S.,
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Maduro, Q.L., Masello, C., Maskell, B., Mastriani, S.D., McLooney, J.C.,
McDowell, C., Pearson, R., Stantipop, S., Thomas, P.J., Touchman, J.W.,
Tsugeon, C., Vogt, J.D., Walker, M.A., Wetherby, K.D., Wiggins, L.,
Young, A., Zhang, L.-H. and Green, E.D.

Clone distribution: MGC clone distribution information can be found
through the I.M.A.G.E. Consortium/LNL at: <http://limage.lnl.gov>
Series: IRAL Plate: 1 Row: c Column: 9
This clone was selected for full length sequencing because it
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FEATURES

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CDS

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| KEYWORDS | RPD3 protein. | | | |
| SOURCE | Homo sapiens (human) | | | |
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| REFERENCE | Eukaryota; Metazoa; Chordata; Craniata; Vertebrate; Euteleostomi; | | | |
| AUTHORS | Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo. | | | |
| TITLE | Furukawa, Y., Kawakami, T., Sudo, K., Inazawa, J., Matsunine, A., | | | |
| JOURNAL | Akizama, T. and Nakamura, Y. | | | |
| MEDLINE | Isolation and mapping of a human gene (RPD3L1) that is homologous | | | |
| PUBMED | to RPD3, a transcription factor in Saccharomyces cerevisiae | | | |
| REFERENCE | Cyogenet. Cell Genet. 73 (1-2), 130-133 (1996) | | | |
| AUTHORS | 96244606 | | | |
| JOURNAL | 8646880 | | | |
| MEDLINE | 2 (bases 1 to 2091) | | | |
| PUBMED | Nakamura, Y. | | | |
| REFERENCE | Unpublished | | | |
| AUTHORS | 3 (bases 1 to 2091) | | | |
| JOURNAL | Nakamura, Y. | | | |
| MEDLINE | Direct Submission | | | |
| PUBMED | Submitted (22-APR-1995) Yusuke Nakamura, Institute of Medical | | | |
| REFERENCE | Science, The University of Tokyo, Laboratory of Molecular Medicine, | | | |
| AUTHORS | Human Genome Center; 4-6-1 Shirokanedai, Minato-Ku, Tokyo 108-8639, | | | |
| JOURNAL | Japan (E-mail: y-daigo@ims.u-tokyo.ac.jp, Tel: 03-5449-5372, | | | |
| MEDLINE | Fax: 03-5449-5433) | | | |
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AR012007
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ACCESSION AR012007
VERSION AR012007.1 GI:3969997
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 2111)
AUTHORS Nakamura, Y. and Furukawa, Y.
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DEFINITION cDNA encoding human transcriptional control protein, RPD.
ACCESSION E11455
VERSION E11455.1 GI:22025091
KEYWORDS JP 1996140687-A/1.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 2111)
AUTHORS Nakamura, Y. and Furukawa, Y.
TITLE RPD, PROTEIN AND DNA ENCODING FOR THE SAME
JOURNAL Patent: JP 1996140687-A 1 04-JUN-1996;
JAPAN FOUND CANCER RES; EISAI CO LTD
COMMENT OS Homo sapiens (human)
PN JP 1996140687-A/1
PD 04-JUN-1996
PF 20-JUL-1995 JP 1995183763
PI 22-SEP-1994 JP 94P 227876
PT NAKAMURA YOSUKE, FURUKAWA YOICHI
PC C12N15/09, C07K14/39, C07K16/18, C12P21/02, C12P21/08, C12Q1/68, PC
(C12P21/02,
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BASE COUNT 572 a 485 c 544 g 510 t
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Best Local Similarity 99.3%; Pred. No. 0;
Matches 1504; Conservative 0; Mismatches 10; Indels 0; Gaps 0;
Qy 97 GGGAGGCGAGCAAGATGGCGAGACGACAGGCGACCCGAGAGAAAGTCTGTACTACTACG 156

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Db 50 GGGAGGCGAGCAAGATGGCGAGACGACAGGCGACCCGAGAGAAAGTCTGTACTACTACG 109
Qy 157 ACCGGGAGTGTGAAATTAATTAATTAATGAACAAGCCACCAATGAAGCCACCGAATCC 216
Db 110 ACCGGGAGTGTGAAATTAATTAATTAATGAACAAGCCACCAATGAAGCCACCGAATCC 169
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Db 170 GCATGACTCAATTTGCTGCTCACTAGTGTCTTACCCGAAAAATGAAATATATGCC 229
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Db 290 TGGGCTCCATCGGTCGAGATACATGCGGAGTACAGCAAGATGACAGATTCACAG 349
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| Qy | 1297 | AGGACGAAGAAGACGACCCCTGACAAAGGCGCATCTGATCTGCTCTGACAAAGAAATGGCT | 1356 |
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| Db | 1370 | ACTCTAAAAAAGCCCAAGAGAGTCAAAACAGAGATGAAAAAGAAAAAGAACCCCAAGAGAGA | 1429 |
| Qy | 1477 | AGAAAGAAATCACCGAANAGAGAAAGAAACCAAGAGAGAGAAACCCCAAGAACCAAGGGGTCA | 1536 |
| Db | 1430 | AGAAAGAAAGTCAACCGAAGAGAGAAAGAAACCAAGAGAGAGAAACCCCAAGAACCAAGGGGTCA | 1489 |
| Qy | 1537 | AGGAGAGAGGCGCAAGTGGCTGTAATGAGACTCTCAAGCTCTGGCTTCCTGCTGAGTCCCT | 1596 |
| Db | 1490 | AGGAGAGAGTCAAGTGGCTGTAATGAGACTCTCAAGCTCTGGCTTCCTGCTGAGTCCCT | 1549 |
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| Db | 1550 | CACGTTTCTTCCCC 1563 | |
| RESULT | 8 | | |
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| DEFINITION | Sequence 2 from patent US 5659016. | | |
| ACCESSION | 162388 | | |
| VERSION | 162388.1 | GI:2480336 | |
| KEYWORDS | | | |
| SOURCE | Unknown. | | |
| ORGANISM | Unknown. | | |
| REFERENCE | 1 (bases 1 to 2111) | | |
| AUTHORS | Nakamura,Y. and Furukawa,Y. | | |
| TITLE | RPDL protein and DNA encoding the same | | |
| JOURNAL | Patent: US 5659016-A 2 19-AUG-1997; | | |
| FEATURES | location/Qualifiers | | |
| source | 1..2111 | | |
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| Qy | 157 | ACGGGGATGTTGGAAATTACTATTATGACAAAGCCACCCCAATGAAAGCTTACCGGATCC | 216 |
| Db | 110 | ACGGGGATGTTGGAAATTACTATTATGACAAAGCCACCCCAATGAAAGCTTACCGGATCC | 169 |
| Qy | 217 | GCATGACTCATTAATTGCTGCTGCACATATGCTCTTACCGAAAAATGGAATCTATGGCC | 276 |
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| Qy | 277 | CTCACAAAAGCCAAATGCTGAGAGAGATGACCAAGTACACAGCGATGACTACATTAATTTCT | 336 |
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| Db | 350 | TTGGTGAAGACTGTCCAGTATTGCATGGCCCTGTTGAGTTCTGTCACTGTCTTACTGGTG | 409 |
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| QY | 1357 | GTCGAGGAAGATTCTCCGATTTCTGAAGAGAGGAGAGGGGGGCGCAGAACTTTTCCA | 1416 |
| Db | 1310 | GTCGAGGAAGATTCTCCGATTTCTGAAGAGAGGAGAGGGGGGCGCAGAACTTTTCCA | 1369 |
| QY | 1417 | ACTTCAAAAAAGCCAAAGAGTCAAAACAGAGATGAAAAAGAAAGAACCCCAAGAGAGA | 1476 |
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RESULT 10
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DEFINITION X98207
VERSION X98207.1 GI:1771285
KEYWORDS histone deacetylase.
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ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1
AUTHORS Bartl S., Taplick J., Lagger G., Khier H., Kuchler K. and Seiser C.
TITLE Identification of mouse histone deacetylase 1 as a growth
factor-inducible gene
JOURNAL Mol. Cell. Biol. 17 (9), 5033-5043 (1997)
MEDLINE 97415582
PUBMED 9271381
REFERENCE 2 (bases 1 to 1977)
AUTHORS Seiser C.
TITLE Direct Submission
JOURNAL Submitted (30-MAY-1996) C. Seiser, University of Vienna, Institute
of Molecular Biology, Vienna Biocenter, Dr.Bohr-Gasse 9, A-1030
Vienna, AUSTRIA
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QY 214 TCGGATGATCATTAATTTGTCTGCTCAATATGCTCTCAACCGAAAAATGAAATCTATC 273
DB 121 TCGGATGATCATTAATTTGTCTGCTCAATATGCTCTCAACCGAAAAATGAAATCTATC 180
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DB 181 GCCCTCAAAAGCCAAATGCTGAGAGATGACCAAGTACCAAGCATGATGATGATCAATTAAT 240
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DB 541 TTGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 600
QY 694 CTGTGCTCTTTCAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 753
DB 601 CTGTGCTCTTTCAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 660
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DB 661 GGGCTGGGCAAGCAAGTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 720
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DB 721 AGTCTATAGAGCCATTTTCAAGCGGATCATGCAAGTAAATTAATTAATTAATTAATTAAT 780
QY 874 GTGCGGTGCTTAAAGTGTGCTCAAGTCTCTTATGAGGATGAGTAAAGTGTGCTTAA 933
DB 781 GTGCGGTGCTTAAAGTGTGCTCAAGTCTCTTATGAGGATGAGTAAAGTGTGCTTAA 840

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Qy 934 ATCTATCATCAAGACACGCCAAGTGTGTGAATTTGTCAAGAGCTTTAACTCGCTTA 993
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Qy 994 TGTGTATGCTGGAGGCGGTGTGTATCAACATTGCTTAACGTTGCCGCTGACATATG 1053
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Qy 1054 AGACAGCTGGGCGCTGGATACGAGATCCCTATGAGCTTCCATACAACTACTACTTTG 1113
Db 961 AATGAGCGGTGGCGCTGGACACAGAGATCCCTATGAGCTTCCCTACAACTACTACTTTG 1020
Qy 1114 AATGCTTTGACACGATTTTCAAGCTTCCATCACTGCTCTTCCATATATGATCAACAGACA 1173
Db 1021 AATGCTTTGACCGGATTTTCAAGCTTCCATCACTGCTCTTCCATATATGATCAACAGACA 1080
Qy 1174 CGATGAGTACTGTGAGAGATCAACAGGACCTGTTGAGAACCTTAAGATGCTGCCGC 1233
Db 1081 CTAAAGAGTACTGTGAGAGATCAACAGGACCTGTTGAGAACCTTAAGATGCTGCCGC 1140
Qy 1234 ACGGACCTGGGCTCCAAACGAGGCGATTTCTGAGGACCGCATCCCTGAGGAGAGTGGCG 1293
Db 1141 ATGCCCCGTGGGCTCCAGTGAAGGCGATCCCTGAGGAGCGCATCCCGAAGAGTGGCG 1200
Qy 1294 ATGAGGACGAGAGGACCTGTGACAGGCGATCTGATCTGCTCTCTGACAAAGAAATG 1353
Db 1201 ATGAGGATGAGAGAGGACCTGTGACAAAGCGATCTGATCTGCTCTGATTAAGCAATG 1260
Qy 1354 CTTGTGAGAGAGATTCTCCGATTTCTGAGAGAGAGAGGAGGCGCGCAAGACTCTT 1413
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RESULT 11
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DEFINITION Mus musculus putative histone deacetylase (Hdi) mRNA, partial cds.
ACCESSION U80780
VERSION U80780.1 GI:2347179
KEYWORDS
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE
AUTHORS Johnson,C.A., White,D., O'Neill,L.P. and Turner,B.M.
TITLE Putative histone deacetylase Hdi from M. musculus
JOURNAL Unpublished
2 (bases 1 to 1999)
AUTHORS Johnson,C.A., White,D., O'Neill,L.P. and Turner,B.M.
TITLE Direct Submission
JOURNAL Submitted (02-DEC-1996) Department of Anatomy, University of Birmingham, Birmingham B15 2TT, U.K.
COMMENT On Sep 2, 1997 this sequence version replaced gi:1737470.
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Matches 1344; Conservative 2; Mismatches 163; Indels 1; Gaps 1;

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6 15..1463
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16 GKRYAVNYPRLDIDDESYEAFPKPMSKVMEMFOSAVLVOCGSDLSGDRICFNL
17 TKGNAKCYEIVKSPNLPMIMGGGGITRANVAKCTYETNALDTRIEPLEYNDYF
18 EYGPDPKLIHSPSNMNTONTYELKIKORLEPNLRLPHAGVOMQALPEDAIBE
19 SGDEDEDEPKRISICSDRIACEEFSDSESGRGNNSNFKKAKVKTDEKE
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21
22 Qy 97 GGGAGCGGACCAAGATGCGCCAGACCGGAGGACCCGGAGAGAAAGTCTGTACTACTACG 156
23 Db 1 GGGCGGGAGCAAGATGCGCCAGACCTCAGGGCACCAAGAGAAAGTCTGTACTACTACG 60
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25 Qy 157 ACGGGAGTGTGAAATTAATTAATGAGCAAGAGCCCAATGAAGCTCAGCAATCC 216
26 Db 61 ACGGGAGTGTGAAATTAATTAATGAGCAAGAGCCCAATGAAGCTCAGCAATCC 120
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55 Qy 757 CTGGCAAGACAGATTTATGTTTAACTACCGGCTCGAGAGCGGAGATTGATGACAGAT 816

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[illegible]

REFERENCE
AUTHORS

1 (bases 1 to 252509)
 Muzyu, D.M., Adams, C., Adio-Oduola, B., Ali-osman, F.R., Allen, C.,
 Alsbrooks, S.L., Amaralunga, H.C., Aye, J.R., Ayelo, M., Banks, T.,
 Barabara, J., Benton, J., Bimge, K., Blankenburg, K., Bonnah, D.,
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 Chen, G., Chen, R., Chen, Z., Chowhry, I., Christopoulos, C.,
 Cleveland, C.D., Cox, C., Coyle, M.D., Dathorne, S.R., David, R.,
 Davila, M.L., Davis, C., Davy-Carroll, L., Dederich, D.A.,
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 Douthwaite, K.J., Draper, H., Dugan-Rocha, S., Durbin, K.J.,
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 Weinstock, G., and Gibbs, R.

TITLE
JOURNAL
REFERENCE
AUTHORS
TITLE
JOURNAL

Submitted (23-OCT-2001) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
3 (bases 1 to 252509)

REFERENCE
AUTHORS
TITLE
JOURNAL

COMMENT

The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas (<http://www.hscg.bcm.tmc.edu/projects/rat/>). Each contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence may extend beyond the ends of the clone and there may be sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence only contigs will be indicated in the feature table.

----- genome center
Center: Baylor College of Medicine
Center code: BCM
Web site: <http://www.hgsc.bcm.tmc.edu>
Contact: hgsc-help@bcm.tmc.edu


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----- Project Information
Center project name: TULM
Center clone name: CH230-2A17
----- Summary Statistics
Assembly program: Phrap, version 0.990329
Consensus quality: 232672 bases at least Q40
Consensus quality: 234784 bases at least Q30
Consensus quality: 236074 bases at least Q20
Estimated insert size: 238642; sum-of-coverage estimation
Quality coverage: 7x in Q20 bases; sum-of-coverage estimation

* NOTE: Estimated insert size may differ from sequence length
* (see http://www.hgsc.bcm.tmc.edu/docs/genbank_draft_data.html).
* NOTE: This is a 'working draft' sequence. It currently
* consists of 2 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.

* 1 248868: contig of 248868 bp in length
* 248869 248968: gap of unknown length
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Best local similarity 88.9%; Pred. No. 0;
Matches 1349; Conservative 0; Mismatches 162; Indels 7; Gaps 2;

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Qy 215 CGGATGATCATTAATTTGCTGCTCAACTATGCTCTTACCGAAATATGAATCTATCG 274
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Db 75379 CTTGCGCTCATCCGCTCCAGATTAATGCTGGAGTACAGAACAGATGAGAGATTCA 75438
Qy 395 CGTTGGAGAGACGTCAGTATTCGATGAGCTGTTGAGTTCGTCAGTTGCTACTG 454
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[illegible]

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REFERENCE AUTHORS TITLE
JOURNAL Direct Submission
Unpublished
2 (bases 1 to 253360)
Morley,K.C.
Direct Submission
Submitted (03-OCT-2001) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
3 (bases 1 to 253360)
Morley,K.C.
Direct Submission
Submitted (13-NOV-2002) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
On Nov 13, 2002 this sequence version replaced gi:23664830.
The sequence in this assembly is a combination of BAC based reads
and whole genome shotgun sequencing reads assembled using Atlas
(http://www.hgsc.bcm.tmc.edu/projects/rat/). Each contig described
in the feature table below represents a scaffold in the Atlas
assembly ('a','contig-scaffold'). Within each contig-scaffold,
individual sequence contigs are ordered and oriented, and separated
by sized gaps filled with Ns to the estimated size. The sequence
may extend beyond the ends of the clone and there may be sequence
contigs within a contig-scaffold that consist entirely of whole
genome shotgun sequence reads. Both end sequences and whole genome
shotgun sequence only contigs will be indicated in the feature
table.

----- Genome Center
Center: Baylor College of Medicine
Center code: BCM
Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu
----- Project Information
Center project name: TUNY
Center clone name: CH230-2C19
----- Summary Statistics
Assembly program: Phrap; version 0.990329
Consensus quality: 235451 bases at least Q40
Consensus quality: 237249 bases at least Q30
Consensus quality: 238382 bases at least Q20
Estimated insert size: 238893; sum-of-contigs estimation
Quality coverage: 6x in Q20 bases; sum-of-contigs estimation

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* NOTE: Estimated insert size may differ from sequence length
* (see http://www.hgsc.bcm.tmc.edu/docs/genbank_draft_data.html) .
* NOTE: This is a 'working draft' sequence. It currently
* consists of 4 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
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* 1 248409: contig of 248409 bp in length
* 248410 248509: gap of unknown length
* 248510 249588: contig of 1079 bp in length
* 249589 249688: gap of unknown length
* 249689 251319: contig of 1631 bp in length
* 251320 251419: gap of unknown length
* 251420 253360: contig of 1941 bp in length.
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/clone="CH230-2C19"
1. 1149
/note="wgs_end_extension
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1200..2271
/note="wgs_end_extension

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AUTHORS
TITLE
JOURNAL
REFERENCE
AUTHORS
JOURNAL
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

Wilson, R.K.
The sequence of Mus musculus clone
Unpublished
2 (bases 1 to 181964)
McPherson, J.D. and Waterston, R.H.
Direct Submission
Submitted (24-JUL-2002) Genome Sequencing Center, 4444 Forest Park
Parkway, St. Louis, MO 63108, USA
3 (bases 1 to 181964)
Wilson, R.K.
Direct Submission
Submitted (30-MAY-2003) Genome Sequencing Center, 4444 Forest Park
Parkway, St. Louis, MO 63108, USA
On May 29, 2003 this sequence version replaced gi:22475688.

----- Genome Center -----
Center: Washington University Genome Sequencing Center
Center code: WUSC
Web site: <http://genome.wustl.edu/gsc/index.shtml>
Contact: submissions@wustl.edu
----- Project Information -----
Center project name: M_BA0430E12
----- Summary Statistics -----
Sequencing vector: M13; 0%
Sequencing vector: plasmid; 100%
Chemistry: Dye-Primer ET; 0% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.990319
Consensus quality: 180253 bases at least Q40
Consensus quality: 180732 bases at least Q30
Consensus quality: 181043 bases at least Q20

* NOTE: This is a 'working draft' sequence. It currently
* consists of 3 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.

1 40509: contig of 40509 bp in length
* 40510 40609: gap of unknown length
* 40610 89491: contig of 48882 bp in length
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ORIGIN

Query Match 74.2% Score 1195.6; DB 2; Length 181964;
Best Local Similarity 87.7%; Pred. No. 2.5e-307;
Matches 1328; Conservative 0; Mismatches 184; Indels 2; Gaps 2;

94 GCGGGAGCGAGCAAGATGCGCAGACGAGCGGCAACCGGAAAGTCTGTACTACT 153
|||
74900 GCCGGCGGTGAGCAAGATGCGCAGACTCAGGCGCAAGAGGAAATCTGTACTACT 74959
|||
154 ACGAGCGGAGTGTGAATTAATTAATGAGCAAGCGCACCAATGAAGCTTACCGAA 213
|||
74960 ATGATGGGAGCTTGGAATTAATTAATGAGCAAGCGCACCAATGAAGCTTACCGAA 75019

QY 214 TCCGATGACTCATTAATTTGCTGCTCAACTATGATCTTACCGAAAAATGAAATCTATC 273
|||
Db 75020 TCTGATGACTCATTAATTTGCTGCTCAACTATGATGATCTTACCGAAAAATGAAATCTATC 75079
|||
QY 274 GCCCTCAAAAGCCAAATGCTGAGAGATGACCAAGTACCAACAGCATGATTAATTAAT 333
|||
Db 75080 GTCTCAAAAGCCAAATGCTGAGAGATGACCAAGTACCAACAGCATGATTAATTAAT 75139
|||
QY 334 TCTTGCGCTCATCCGTCGATTAACATGTCGAGATGACAGCAAGATGACAGATTTCA 393
|||
Db 75140 TCTTGCTTTTATTAATCAACGATTAATGATGATTAATGACCAAGATGACAGATTTCA 75199
|||
QY 394 ACGTTGAGAGACTGTCAGATTAATGATGATGATGATGATGATGATGATGATGATG 453
|||
Db 75200 ATGTTGATGAGACTGTCGATTTTATGATGATGATGATGATGATGATGATGATGATG 75259
|||
QY 454 GTGCTTCTGAGCAAGTCTGTGAAATTAATTAAGACGACGACGACGATCCGTAAT 513
|||
Db 75260 GAGGCTCTGCGCAAGTCTGTGAAATTAATTAAGACGACGACGACGATCCGTAAT 75319
|||
QY 514 GGGCTGGGGGCTGCAACATGCAAAAGTCCGAGCATGCGCTTCTGTACGTCATG 573
|||
Db 75320 GGGCTGGGGGCTGCAACATGCAAAAGTCCGAGCATGCGCTTCTGTACGTCATG 75379
|||
QY 574 ATATGCTTTGACCATCTGGAACCTGTAAGTATCAACAGAGGTCGTACATTTGACA 633
|||
Db 75380 ACATGCTTTGACCATCTGGAACCTGTAAGTATCAACAGAGGTCGTACATTTGACA 75439
|||
QY 634 TTGATATTCACATGATGACGCGGTGAGAGAGGCTTTTACACGACGACGCGGTCTGA 693
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Db 75440 TTGATATTCACATGATGACGCGGTGAGAGAGGCTTTTACACGATGATGATGATG 75499
|||
QY 694 CTGTCCTTTTCAATGATGAGAGTCTCCAGGATCGGGGACCTTACGGATACG 753
|||
Db 75500 CTGTCCTTTTCAATGATGAGAGTCTCCAGGATCGGGGACCTTACGGATACG 75559
|||
QY 754 GGGCTGCAAAAGCAAGTATTAATGCTGTTAATCAACGCTTCGAGACGAGATTTGATGACG 813
|||
Db 75560 GGGCTGCAAAAGCAAGTATTAATGCTGTTAATCAACGCTTCGAGACGAGATTTGATGACG 75619
|||
QY 814 AGTCTATGAGGCGCATTTTAAAGCGGTCATGTCCAAGTAAAGTAAAGATTTTCAAGCTTA 873
|||
Db 75620 AATCTATGAGGCGCATTTTAAAGCGGTCATGTCCAAGTAAAGTAAAGATTTTCAAGCTTA 75679
|||
QY 874 GTGCGATGCTTACAGTGTGATGATGATGATGATGATGATGATGATGATGATGATG 933
|||
Db 75680 GTGCGATGCTTACAGTGTGATGATGATGATGATGATGATGATGATGATGATGATG 75739
|||
QY 934 ATCTATCTATCAAGAGCAGCGCAAGTGTGAAATTTGTCAAGCTTTAACTGCTTA 993
|||
Db 75740 ATCTATCTATCAAGAGCAGCGCAAGTGTGAAATTTGTCAAGCTTTAACTGCTTA 75799
|||
QY 994 TGCATGATCTGAGAGCGGTGTGTTACCACTTTGTATGATGATGATGATGATGATGATG 1053
|||
Db 75800 TGCATGATCTGAGAGCGGTGTGTTACCACTTTGTATGATGATGATGATGATGATGATGATG 75859
|||
QY 1054 AGACAGCTGTGGCGCTGATACGAGATCTCTATGATGATGATGATGATGATGATGATGATG 1113
|||
Db 75860 AAGACAGCTGTGGCGCTGATACGAGATCTCTATGATGATGATGATGATGATGATGATGATG 75919
|||
QY 1114 AATCTTTGAGCAAGATTTCAAGTCCATCACTCACTCACTCACTCACTCACTCACTCACTCA 1173
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Db 75920 AATCTTTGAGCAAGATTTCAAGTCCATCACTCACTCACTCACTCACTCACTCACTCACTCA 75979
|||
QY 1174 CGAATGATCTGAGAGATTAATCAACAGCGACTGTTTGAACCTTTGAATGTGCGCC 1233
|||
Db 75980 CTAAACAATGATCTGAGAGATTAATCAACAGCGACTGTTTGAACCTTTGAATGTGCGCC 76039
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QY 1234 ACGCACTGGGTTCGAAGCGCGGATCTGAGAGCGCATCTCGAGAGAGTGGCG 1293
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Db 76040 ACGCACTGGGTTCGAAGCGCGGATCTGAGAGCGCATCTCGAGAGAGTGGCG 76099
|||

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OM nucleic - nucleic search, using sw model

Run on: December 5, 2003, 13:00:53 ; Search time 457 Seconds
(without alignments)
9515.962 Million cell updates/sec

Title: US-09-817-913-2

Perfect score: 1611
Sequence: 1 atgtctgggtctctgccgcg.....tccctcagttcttctccccc 1611

Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 2552756 seqs, 1349719017 residues

Total number of hits satisfying chosen parameters: 5105512

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB | ID | Description |
|------------|--------|-------------|--------|----------|--------------------|--------------------|
| 1 | 1610.6 | 100.0 | 1611 | 24 | ABK87715 | Human cDNA encodin |
| 2 | 1596.6 | 99.1 | 22 | AAK89554 | Human histone deac | |
| 3 | 1499.6 | 93.1 | 2163 | AAK16188 | Human prostate can | |
| 4 | 1499.6 | 93.1 | 2378 | ABV25106 | Human prostate exp | |
| 5 | 1498 | 93.0 | 2091 | AAK40884 | Human histone deac | |
| 6 | 1498 | 93.0 | 2091 | ABK83674 | Human cDNA differe | |
| 7 | 1498 | 93.0 | 2111 | AAK12940 | RPD1 transcription | |
| 8 | 1436.2 | 89.1 | 1671 | ABK58329 | DNA encoding TAR-d | |

| | | | | | | |
|----|--------|------|------|----|-----------|--------------------|
| 9 | 1434.6 | 89.1 | 1449 | 18 | AAK86371 | cDNA encoding a hi |
| 10 | 1433.4 | 89.0 | 1674 | 23 | ABK58325 | DNA encoding HDAC1 |
| 11 | 1378 | 85.5 | 1582 | 25 | AAK81302 | DNA encoding novel |
| 12 | 818 | 50.8 | 1997 | 24 | AB199512 | Mouse ischaemic co |
| 13 | 805.2 | 50.0 | 1985 | 20 | AAK23066 | Human MERT2 relate |
| 14 | 805.2 | 50.0 | 1985 | 22 | AAK90323 | U31814 cDNA clone. |
| 15 | 805.2 | 50.0 | 1985 | 22 | AAK89555 | Human histone deac |
| 16 | 805.2 | 50.0 | 1985 | 22 | AAK50181 | Breast cancer asso |
| 17 | 805.2 | 50.0 | 1985 | 25 | ABK34831 | Coding sequence SE |
| 18 | 795.6 | 49.4 | 1985 | 24 | ABK87716 | Human cDNA encodin |
| 19 | 729 | 45.3 | 2145 | 23 | ABL01897 | Drosophila melanog |
| 20 | 640.6 | 39.8 | 4755 | 23 | ABL01896 | Drosophila melanog |
| 21 | 502.6 | 31.2 | 1943 | 20 | AAK90840 | Maize histone deac |
| 22 | 501.8 | 31.1 | 2019 | 20 | AAK90839 | Maize histone deac |
| 23 | 501.6 | 31.1 | 680 | 25 | AAK28310 | Toxicologically re |
| 24 | 499.6 | 31.0 | 1990 | 21 | AAZ58259 | Rice histone deace |
| 25 | 498.2 | 30.9 | 1807 | 22 | AAK80350 | Nucleotide sequenc |
| 26 | 480.2 | 29.8 | 1935 | 25 | ABK63632 | Human cDNA #632 di |
| 27 | 480.2 | 29.8 | 1954 | 22 | AAK89556 | Human histone deac |
| 28 | 480.2 | 29.8 | 1954 | 24 | ABK87717 | Human cDNA encodin |
| 29 | 477 | 29.6 | 1805 | 21 | AAZ58260 | Soybean histone de |
| 30 | 460.8 | 28.6 | 1576 | 20 | AAK90841 | Maize histone deac |
| 31 | 459 | 28.5 | 1826 | 20 | AAK90837 | Maize histone deac |
| 32 | 450.2 | 27.9 | 455 | 24 | ABK87577 | Human colon cancer |
| 33 | 434 | 26.9 | 1662 | 23 | ABL04121 | Drosophila melanog |
| 34 | 433.4 | 26.9 | 1609 | 21 | AAK46043 | Arabidopsis thalia |
| 35 | 433.4 | 26.9 | 1611 | 21 | AAK33022 | Arabidopsis thalia |
| 36 | 431.8 | 26.8 | 1800 | 22 | AAK80351 | Nucleotide sequenc |
| 37 | 413 | 25.6 | 586 | 22 | AAK25097 | Human ovarian PCR- |
| 38 | 413 | 25.6 | 586 | 22 | AAK83742 | Human ovarian tumo |
| 39 | 402 | 25.0 | 576 | 22 | AAK25098 | Human ovarian PCR- |
| 40 | 402 | 25.0 | 576 | 22 | AAK83743 | Human ovarian tumo |
| 41 | 395.4 | 24.5 | 680 | 21 | ABK06268 | Human colon cancer |
| 42 | 392.4 | 24.4 | 600 | 21 | AAK16397 | Human colon cancer |
| 43 | 386.8 | 24.0 | 402 | 22 | AAK55632 | Human breast tumo |
| 44 | 369 | 22.9 | 3793 | 23 | ABL04120 | Drosophila melanog |
| 45 | 353.4 | 21.9 | 650 | 24 | ABK060010 | Human colon cancer |

ALIGNMENTS

| RESULT | ID | ABK87715 | standard; cDNA; 1611 Bp. |
|--------|----|---|--------------------------|
| XX | XX | ABK87715 | |
| XX | XX | ABK87715 | |
| XX | XX | 07-OCT-2002 (first entry) | |
| DE | XX | Human cDNA encoding Histone deacetylase isoform 1. | |
| XX | XX | Human; ss; gene; histone deacetylase; HDAC-1; cancer; cytostatic; | |
| KW | KW | antitumor; tumour suppressor; cell proliferation; tumour; | |
| KW | KW | programmed cell death; necrotic cell death. | |
| XX | XX | Homo sapiens. | |
| OS | OS | Homo sapiens. | |
| XX | XX | Location/Qualifiers | |
| FT | FT | Key | |
| FT | FT | CDS | |
| FT | FT | 111..1559 | |
| FT | FT | /*tag= a | |
| FT | FT | /product= "HDAC-1" | |
| FT | FT | /transl_except= (pos:750..757,aa:Ile) | |
| FT | FT | /transl_except= (pos:765..767,aa:Gly) | |
| FT | FT | /transl_except= (pos:783..788,aa:Tyr) | |
| FT | FT | /transl_except= (pos:939..941,aa:Thr) | |
| FT | FT | /transl_except= (pos:1251..1253,aa:Met) | |
| FT | FT | /transl_except= (pos:1482..1487,aa:Glu-Val) | |
| FT | FT | /transl_except= (pos:1545..1547,aa:Val) | |
| XX | XX | US2002061860-A1. | |
| XX | XX | 23-MAY-2002. | |

XX 06-AUG-2001; 2001US-0817913.
XX
XX 24-MAR-2000; 2000US-192157P.
XX
XX (LIZZ/) LI Z.
XX (BONF/) BONFILS C.
XX (BEST/) BESTERMAN J.
XX
XX LI Z, Bonfils C, Besterman J;
XX
XX WPI: 2002-507650/54.
XX P-PSDB; AAU99656.
XX
XX Agent that specifically inhibits an isoform of histone deacetylase,
XX useful for treating cancer and other cell proliferative diseases,
XX preferably comprises an antisense oligonucleotide -
XX
XX Claim 6; Fig 1B; 60pp; English.
XX
XX The invention relates to an agent that inhibits an isoform of histone
XX deacetylase (HDAC-1 to HDAC-8) but not all isoforms, e.g., an
XX antisense oligonucleotide. Also included are inhibiting an HDAC isoform
XX in a cell by treatment with the agent, identifying an HDAC isoform that
XX is required for induction of cell proliferation or differentiation and
XX inhibiting cell proliferation by treatment with two antisense
XX oligonucleotides or small molecules that inhibit a specific HDAC
XX isoform, or antisense oligonucleotide or small molecules that inhibit
XX DNA methyltransferase. The agent therefore acts as a tumour suppressor.
XX The agents are used to treat diseases of cell proliferation and
XX differentiation (e.g cancer and tumours), by inducing growth retardation,
XX cell proliferation in humans. The agents are selective for particular
XX isoforms, compared to known inhibitors which are not selective.
XX The present sequence encodes the HDAC-1 isoform.
XX
SQ Sequence 1611 BP; 428 A; 389 C; 439 G; 354 T; 1 other;
Query Match 100.0%; Score 1610.6; DB 24; Length 1611;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1611; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ATGCTGGGGGCTCTGCGCCGCTGGGCTGTCTGCCACTCGGTCATCTGAGAACCA 60
Db 1 ATGCTGGGGGCTCTGCGCCGCTGGGCTGTCTGCCACTCGGTCATCTGAGAACCA 60
QY 61 GCCTGAGCGRCTCTGTCACTCGGGGTAGACCACGCGGGAGCGAGCAAGATGGCGAGA 120
Db 61 GCCTGAGCGRCTCTGTCACTCGGGGTAGACCACGCGGGAGCGAGCAAGATGGCGAGA 120
QY 121 CGCAGGGGACCCCGAGGAAAGTCTGTACTACTAGACGGGGAGTGGAAATTAATTA 180
Db 121 CGCAGGGGACCCCGAGGAAAGTCTGTACTACTAGACGGGGAGTGGAAATTAATTA 180
QY 181 ATGGAACAAGGCGACCAATGAAGGCTCAACGGAATCCGATGACTCATTAATTTGCTGCA 240
Db 181 ATGGAACAAGGCGACCAATGAAGGCTCAACGGAATCCGATGACTCATTAATTTGCTGCA 240
QY 241 ACTATGCTCTTACCGAAAAATGAAATCTATCGCCCTCAACAAAGCCATGCTGAGAGA 300
Db 241 ACTATGCTCTTACCGAAAAATGAAATCTATCGCCCTCAACAAAGCCATGCTGAGAGA 300
QY 301 TGACCAAGTACCAACGCGATGACTTAATTAATTTGCGCTCAATCCGTCAGATAACA 360
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QY 361 TGTGGAGTACAGCAAGAGATGCAAGATTCACAGTTGAGAGACGTCAGATTTCG 420
Db 361 TGTGGAGTACAGCAAGAGATGCAAGATTCACAGTTGAGAGACGTCAGATTTCG 420
QY 421 ATGGCCTGTTGAGTTCTGTCAAGTGTCTACTGAGTGTCTGTGAGCAAGTCTGAAAC 480
Db 421 ATGGCCTGTTGAGTTCTGTCAAGTGTCTACTGAGTGTCTGTGAGCAAGTCTGAAAC 480

QY 481 TTAATAAGCAGACAGGACATCGCCGTGAATTGGGCTGGGGGCTTGACCATGCAAGA 540
Db 481 TTAATAAGCAGACAGGACATCGCCGTGAATTGGGCTGGGGGCTTGACCATGCAAGA 540
QY 541 AGTCGAGGATCTGGCTTCTGTAGCTCAATGATATCGTCTTGGCCATCTGGAACTGC 600
Db 541 AGTCGAGGATCTGGCTTCTGTAGCTCAATGATATCGTCTTGGCCATCTGGAACTGC 600
QY 601 TAAAGTATCACAGAGGCTGTATGATGATGATATATGATGATGATGATGATGATG 660
Db 601 TAAAGTATCACAGAGGCTGTATGATGATGATGATGATGATGATGATGATGATGATG 660
QY 661 AAGAGGCTTCTACACACAGGACCGGGTCACTGCTGCTTCAATTAATGAGAGT 720
Db 661 AAGAGGCTTCTACACACAGGACCGGGTCACTGCTGCTTCAATTAATGAGAGT 720
QY 721 ACTTCCAGGACCTGGGACCTTACGGGATACCGGGGCTGGCAAGCAAGTATTAATGCTG 780
Db 721 ACTTCCAGGACCTGGGACCTTACGGGATACCGGGGCTGGCAAGCAAGTATTAATGCTG 780
QY 781 TTAATTAACCGCTCCGAGACGGGATGATGACGATCTTATGAGGCTATTTCAAGCCG 840
Db 781 TTAATTAACCGCTCCGAGACGGGATGATGACGATCTTATGAGGCTATTTCAAGCCG 840
QY 841 TCAATGCCAAGTAATGAGATGTTCCAGCTGTGCGGCTTACAGTGTGCTCAG 900
Db 841 TCAATGCCAAGTAATGAGATGTTCCAGCTGTGCGGCTTACAGTGTGCTCAG 900
QY 901 ACTCCATATCGGGAGATCGGTAGTGTCTTCAATCTATCTATCAAGACAGCCCAAGT 960
Db 901 ACTCCATATCGGGAGATCGGTAGTGTCTTCAATCTATCTATCAAGACAGCCCAAGT 960
QY 961 GTGTGAATTTGTAAGAGCTTTAACTGCTTATGCTGATGCTGGAGCGGTGTTACA 1020
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QY 1021 CCAATGGTAAGTGTGCGCGGTGCGACATATGACAGCTGTGGCCTGATACGAGA 1080
Db 1021 CCAATGGTAAGTGTGCGCGGTGCGACATATGACAGCTGTGGCCTGATACGAGA 1080
QY 1081 TCCCTAATGAGCTTCCATATGATGATCTTGAATCTTTGGAACAGATTTCAAGCTCC 1140
Db 1081 TCCCTAATGAGCTTCCATATGATGATCTTGAATCTTTGGAACAGATTTCAAGCTCC 1140
QY 1141 ACATCACTCTTCCATATGATGATCTTGAATCTTTGGAACAGATTTCAAGCTCC 1200
Db 1141 ACATCACTCTTCCATATGATGATCTTGAATCTTTGGAACAGATTTCAAGCTCC 1200
QY 1201 AGGACCTGTTGAAGACCTTGAAGTGTGCGCGACGACCTGGGGGTCAAGCGAGCGA 1260
Db 1201 AGGACCTGTTGAAGACCTTGAAGTGTGCGCGACGACCTGGGGGTCAAGCGAGCGA 1260
QY 1261 TTCCTGAGAGCGCATCTCTGAGAGAGTGGCATGAGAGAGAGAGAGAGAGAGAGAG 1320
Db 1261 TTCCTGAGAGCGCATCTCTGAGAGAGTGGCATGAGAGAGAGAGAGAGAGAGAGAG 1320
QY 1321 GCATCTGATCTGCTCTCTGACAAAGAAATGCTGTGAGAGAGATTTCCGATTTCTG 1380
Db 1321 GCATCTGATCTGCTCTCTGACAAAGAAATGCTGTGAGAGAGATTTCCGATTTCTG 1380
QY 1381 AAG 1440
Db 1381 AAG 1440
QY 1441 AAACAGAGATGAAAAAG 1500
Db 1441 AAACAGAGATGAAAAAG 1500
QY 1501 AAACAG 1560
Db 1501 AAACAG 1560

| | | | | |
|-----------------|-------------|---------------|---|------|
| Oy | | 1381 | AAGAGGAGGGGAGAGGGGGCCGCCAAGAATCTTTCACACTTTCAAAAAAAACCAGAGAGTCA | 1440 |
| Dd | | 1381 | AAGAGGAGGGGAGAGGGGGCCGCCAAGAATCTTTCACACTTTCAAAAAAAACCAGAGAGTCA | 1440 |
| Oy | | 1441 | AAACAGAGGAATGAAAAGAAAAGAAAAGCACAAGAGAGAAAAGATCACCGAAGAGAGA | 1500 |
| Dd | | 1441 | AAACAGAGGAATGAAAAGAAAAGAAAAGCACAAGAGAGAAAAGATCACCGAAGAGAGA | 1500 |
| Oy | | 1501 | AAACCAAGAGAGAGAAAGCCCAAGCCAAAGGGGTCAAGAGAGAGGCCCAAATTGGCTTGAA | 1560 |
| Dd | | 1501 | AAACCAAGAGAGAGAAAGCCCAAGCCAAAGGGGTCAAGAGAGAGGCCCAAATTGGCTTGAA | 1560 |
| Oy | | 1561 | TGAGCCTTCAGAGCTGCCTTCCTCCGCTGAGAGCCCTCAGTGTTTTCTTTCCCC | 1611 |
| Dd | | 1561 | TGAGCCTTCAGAGCTGCCTTCCTCCGCTGAGAGCCCTCAGTGTTTTCTTTCCCC | 1611 |
| RESULT 3 | | | | |
| XX | AAF16188 | ID | AAF16188 standard; cDNA; 2163 BP. | |
| XX | AAF16188; | | | |
| XX | 13-MAR-2001 | (first entry) | | |
| DE | | | Human prostate cancer antigen nucleotide sequence SEQ ID NO:623. | |
| KW | | | Human; prostate cancer; prostate cancer antigen; detection; diagnosis; | |
| KM | | | neuroprotective; cytoprotic; cardioactive; immunomodulatory; muscular; | |
| KW | | | vulnerable; gastrointestinal; nephrotoxic; antiinfective; gynaecological; | |
| KM | | | antibacterial; gene therapy; neural; immune; reproductive; renal; | |
| KW | | | gastrointestinal; pulmonary; cardiovascular; proliferative disorder; | |
| KM | | | wound; infectious disease; ss. | |
| XX | | | Homo sapiens. | |
| OS | | | | |
| XX | | | MO200055174-A1. | |
| FN | | | 21-SEP-2000. | |
| PD | | | | |
| XX | | | 08-MAR-2000; 2000WO-US05988. | |
| Pf | | | | |
| XX | | | 12-MAR-1999; 99US-0124270. | |
| PR | | | | |
| XX | | | (HUMA-) HUMAN GENOME SCI INC. | |
| PA | | | (ROSE/) ROSEN C A. | |
| XX | | | Rosen CA, Ruben SM; | |
| PI | | | | |
| XX | | | WPI; 2000-587513/55. | |
| DR | | | P-PsDB; AAB56985. | |
| DR | | | | |
| XX | | | Prostate cancer associated gene sequences, referred to as prostate | |
| PT | | | cancer antigens, useful for treatment, prevention, and diagnosis of | |
| PT | | | disorders such as prostate cancer - | |
| XX | | | | |
| PS | | | Claim 1; Page 1067-1068; 2338pp; English. | |
| XX | | | | |
| CC | | | AAF15566 to AAF16505 encode the human prostate cancer associated | |
| CC | | | proteins, called prostate cancer antigens, given in AAB56363 to AAB57302. | |
| CC | | | The prostate cancer antigens can have neuroprotective, cytoprotic, | |
| CC | | | cardioactive, immunomodulatory, muscular, vulnerary, gastrointestinal, | |
| CC | | | nephrotoxic, antiinfective, gynaecological and antibacterial activities, | |
| CC | | | and can be used in gene therapy. The prostate cancer antigen | |
| CC | | | polynucleotides may be used for detection of prostate cancer, chromosome | |
| CC | | | identification, as chromosome markers, and for numerous other diagnostic | |
| CC | | | or research purposes. The prostate cancer antigens may be used to treat | |
| CC | | | disorders such as neural, immune, muscular, reproductive, | |
| CC | | | gastrointestinal, pulmonary, cardiovascular, renal, and proliferative | |
| CC | | | disorders, wounds, and infectious diseases. AAF16506 to AAF16514 to | |
| CC | | | AAB57303 construct sequences used in the exemplification of the present | |
| CC | | | invention. | |

| XX | Sequence | 2163 BP; 606 A; 490 C; 551 G; 515 T; 1 other; |
|----------------------------|--|---|
| Query Match | 93.1%; Score 1499.6; DB 21; Length 2163; | |
| Best Local Similarity | 99.4%; Pred. No. 0; | |
| Matches 1505; Conservative | 0; Mismatches 9; Indels 0; Gaps 0; | |
| QY | 97 | GGGAGGGGAGCAAAATGGCCGACAGCGAGGGCACCCGGAGGAAAGTCGTGACTACTACG 156 |
| Db | 71 | GGGAGGGGAGCAAAATGGCCGACAGCGAGGGCACCCGGAGGAAAGTCGTGACTACTACG 130 |
| QY | 157 | ACGGGGAATGTTGAAATTTACTATTATGAGACAGGCCACCCAAATGAGCCTCCAGAAATCC 216 |
| Db | 131 | ACGGGGAATGTTGAAATTTACTATTATGAGACAGGCCACCCAAATGAGCCTCCAGAAATCC 190 |
| QY | 217 | GCATGACTCATTAATTTGCTGCTCAACTATGCTCTCTACCCGAAAATGGAATCTATGGCC 276 |
| Db | 191 | GCATGACTCATTAATTTGCTGCTCAACTATGCTCTCTACCCGAAAATGGAATCTATGGCC 250 |
| QY | 277 | CTCAAAAGCCAAATGCTGAGAGATGACAAAGTACCAAGAGATGACTACATTAATTTCT 336 |
| Db | 251 | CTCAAAAGCCAAATGCTGAGAGATGACAAAGTACCAAGAGATGACTACATTAATTTCT 310 |
| QY | 337 | TGCGCTCCATCCGCTCCAGATTAACATGTGCGAGTACAGCAAGCAGATGCAGATTTCAACG 396 |
| Db | 311 | TGCGCTCCATCCGCTCCAGATTAACATGTGCGAGTACAGCAAGCAGATGCAGATTTCAACG 370 |
| QY | 397 | TTGGTGAAGACTGTCCAGATATTCCATGAGCGCTGTTGAGTTCTGTCAAGTTGTCTACG 456 |
| Db | 371 | TTGGTGAAGACTGTCCAGATATTCCATGAGCGCTGTTGAGTTCTGTCAAGTTGTCTACG 430 |
| QY | 457 | GTTCTGTGAGCAAGTGTCTGTAACTTAATAAGCAGCAGACGGAATGCGCGTGAATTTGGG 516 |
| Db | 431 | GTTCTGTGAGCAAGTGTCTGTAACTTAATAAGCAGCAGACGGAATGCGCGTGAATTTGGG 490 |
| QY | 517 | CTGGGGGGCTGSCACATGSCAAAGAAAGTCCGAGGATCGGCTTCTGTTACGTCATGATA 576 |
| Db | 491 | CTGGGGGGCTGSCACATGSCAAAGAAAGTCCGAGGATCGGCTTCTGTTACGTCATGATA 550 |
| QY | 577 | TGCTCTTGCGCCATCCTGGAACTGCTTAAGTATCACAGAGGTCGTGACTTGAATTTG 636 |
| Db | 551 | TGCTCTTGCGCCATCCTGGAACTGCTTAAGTATCACAGAGGTCGTGACTTGAATTTG 610 |
| QY | 637 | ATATTACCATGTGTGAGCGGCGTGGAAAGGCGTTCTTACACAGGACCGGCTCATGACTG 696 |
| Db | 611 | ATATTACCATGTGTGAGCGGCGTGGAAAGGCGTTCTTACACAGGACCGGCTCATGACTG 670 |
| QY | 697 | TGTCCTTTCAATAGTATGAGAGTACTTCCAGGAACCTGAGGACCTTACCGGATACCGGGG 756 |
| Db | 671 | TGTCCTTTCAATAGTATGAGAGTACTTCCAGGAACCTGAGGACCTTACCGGATACCGGGG 730 |
| QY | 757 | CTGGCAAAAGCAAGTATTTATGCTGTTAACTACCGGCTCCGAGCGGATGATGATGACGAGT 816 |
| Db | 731 | CTGGCAAAAGCAAGTATTTATGCTGTTAACTACCGGCTCCGAGCGGATGATGATGACGAGT 790 |
| QY | 817 | CCATAAGAGCCATTTTCAAGCGCGGTCAATGTCCAAAGTATGAGAGATGTTCCAGCTTATG 876 |
| Db | 791 | CCATAAGAGCCATTTTCAAGCGCGGTCAATGTCCAAAGTATGAGAGATGTTCCAGCTTATG 850 |
| QY | 877 | CGGTGTGTTTCAAGTGTGCTCAACATCTCCATCTGGGGATCCGTTAGTTGCTTCAATC 936 |
| Db | 851 | CGGTGTGTTTCAAGTGTGCTCAACATCTCCATCTGGGGATCCGTTAGTTGCTTCAATC 910 |
| QY | 937 | TATCATCAAAAGGACAGCCCAAGTGTGGAATTTGCAAGAGCTTTAACTGCTCTATGC 996 |
| Db | 911 | TATCATCAAAAGGACAGCCCAAGTGTGGAATTTGCAAGAGCTTTAACTGCTCTATGC 970 |
| QY | 997 | TGATGCTGGAGGCGGTGTGTACCAATCTGTAAAGTTGCCCGGTGTGTGACATATGAGA 1056 |
| Db | 971 | TGATGCTGGAGGCGGTGTGTACCAATCTGTAAAGTTGCCCGGTGTGTGACATATGAGA 1030 |
| QY | 1057 | CAGCTGTGGCCCTGGATACGAGATCCCTTAATGAGCTTCCATACATGACTACTTTGAAAT 1116 |

Db 1031 CAGCTGTGCGCTCGATAGGAGAGATCCCTAATGAGCTTCCTCAATGACTACTTGTAAAT 1090
 Qy 1117 ACTTTGACCAAGATTTCAAGCTCCACATCATGCTCTTCCATATATGACTTAACAGAACGCA 1176
 Db 1091 ACTTTGACCAAGATTTCAAGCTCCACATCATGCTCTTCCATATATGACTTAACAGAACGCA 1150
 Qy 1177 ATGAGTACTGTGAGAGAGATCAACAGCGACTGTTTGAAGACCTTAGAATGCTGCCGACG 1236
 Db 1151 ATGAGTACTGTGAGAGAGATCAACAGCGACTGTTTGAAGACCTTAGAATGCTGCCGACG 1210
 Qy 1237 CACCTGGGGTCCCAAGCGAGCGATTCCTTGAGAGACCCCTCTTGAGAGAGAGTGGCGATG 1296
 Db 1211 CACCTGGGGTCCCAAGCGAGCGATTCCTTGAGAGACCCCTCTTGAGAGAGAGTGGCGATG 1270
 Qy 1297 AGGACGAGAGCGACCTCGACCAAGCGATTCGATCTGCTCTCTGAACCAAGATGGCT 1356
 Db 1271 AGGACGAGAGCGACCTCGACCAAGCGATTCGATCTGCTCTCTGAACCAAGATGGCT 1330
 Qy 1357 GTGAGGAGAGATTCTCCGATTTGAAAGAGAGAGAGGGGGCGCGAAGACTCTTCCA 1416
 Db 1331 GTGAGGAGAGATTCTCCGATTTGAAAGAGAGAGAGGGGGCGCGAAGACTCTTCCA 1390
 Qy 1417 ACTTCAAAAAAGCGAAGAGATGAAAAAGAGATGAAAAAGAAAAAGCCAGAGAGA 1476
 Db 1391 ACTTCAAAAAAGCGAAGAGATGAAAAAGAGATGAAAAAGAAAAAGCCAGAGAGA 1450
 Qy 1477 AGAAGAGATCAACCGAAGAGAGAGAAAAAGAGAGAGAGAACCGAAGCGCAAGGGGTCA 1536
 Db 1451 AGAAGAGATCAACCGAAGAGAGAGAAAAAGAGAGAGAGAACCGAAGCGCAAGGGGTCA 1510
 Qy 1537 AGGAGAGAGCGCAAGTGGCTGAGATGAGACCTCTCCAGCTCTGCTCTGCTGAGTCCCT 1596
 Db 1511 AGGAGAGAGCGCAAGTGGCTGAGATGAGACCTCTCCAGCTCTGCTCTGCTGAGTCCCT 1570
 Qy 1597 CACGTTCTTTCC 1610
 Db 1571 CACGTTCTTTCC 1584
 RESULT 4
 ABV25106
 ID ABV25106 standard; cDNA; 2378 BP.
 AC ABV25106;
 XX
 DT 16-SEP-2002 (first entry)
 XX
 DE Human prostate expression marker cDNA 25097.
 XX
 KM Human; prostate cancer; cytostatic; carcinogen; pharmacodynamic marker;
 KM pharmacogenomic marker; gene; ss.
 XX
 OS Homo sapiens.
 PN W0200160860-A2.
 XX
 PD 23-AUG-2001.
 PF 20-FEB-2001; 2001WO-US05171.
 XX
 PR 17-FEB-2000; 2000US-183319P.
 PR 16-MAR-2000; 2000US-189862P.
 PR 25-MAY-2000; 2000US-207454P.
 PR 09-JUN-2000; 2000US-211314P.
 PR 18-JUL-2000; 2000US-219007P.
 PR 13-DEC-2000; 2000US-255281P.
 XX
 PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
 XX
 PI Schlegel R, Endege WO, Monahan JR;
 DR WPI; 2001-662795/76.
 XX

PT Novel isolated nucleic acid molecule associated with cancerous state of
 PT prostate cells and correlating with presence of prostate cancer, useful
 PT for detecting presence of prostate cancer, stage of prostate cancer -
 PS Claim 1, Page 4885; 11750pp; English.
 XX
 CC The invention relates to an isolated nucleic acid molecule (1) comprising
 CC a nucleotide sequence given in Tables 1-9 (ABV0010-ABV62213) of the
 CC specification or its complement. (1) is useful for:
 CC (a) assessing whether a patient is afflicted with prostate cancer;
 CC (b) monitoring the progression of prostate cancer in a patient;
 CC (c) assessing the efficacy of a test compound to inhibit prostate
 CC cancer in a patient;
 CC (d) assessing the efficacy of a therapy for inhibiting prostate cancer
 CC in a patient;
 CC (e) selecting a composition for inhibiting prostate cancer in a patient;
 CC (f) assessing the prostate cell carcinogenic potential of a compound;
 CC (g) determining whether prostate cancer has metastasized in a patient;
 CC (h) assessing the aggressiveness or indolence of prostate cancer in a
 CC patient;
 CC (i) is also useful as a pharmacodynamic or pharmacogenomic marker.
 XX
 SQ Sequence 2378 BP; 659 A; 559 C; 619 G; 541 T; 0 other;
 Query Match 93.1%; Score 1499.6; DB 23; Length 2378;
 Best Local Similarity 99.4%; Pred. No. 0;
 Matches 1505; Conservative 0; Mismatches 9; Indels 0; Gaps 0;
 Qy 97 GGGAGCGAGCAAGATGCGCGAGAGCGCAAGCGAGAGAAAGTCTTTACTACTACG 156
 Db 76 GGGAGCGAGCAAGATGCGCGAGAGCGCAAGCGAGAGAAAGTCTTTACTACTACG 135
 Qy 157 AGGGGAGTTGGAAATTACTATTATGACCAAGGCAACCAATGAAAGCTCAACCGAATCC 216
 Db 136 AGGGGAGTTGGAAATTACTATTATGACCAAGGCAACCAATGAAAGCTCAACCGAATCC 195
 Qy 217 GCATGACTCATATTGCTGCTCAACTATGCTCTCAACGGAATGAAATCTATCGCC 276
 Db 196 GCATGACTCATATTGCTGCTCAACTATGCTCTCAACGGAATGAAATCTATCGCC 255
 Qy 277 CTCACAAAGCCAAATGCTGAGAGATGACCAAGTACCAAGCATGACTTAATTAATTC 336
 Db 256 CTCACAAAGCCAAATGCTGAGAGATGACCAAGTACCAAGCATGACTTAATTAATTC 315
 Qy 337 TGGCTCCATCCGCTCCAGATAATCATGTCGATGACGAAGAGAGAGATTAAG 396
 Db 316 TGGCTCCATCCGCTCCAGATAATCATGTCGATGACGAAGAGAGATTAAG 375
 Qy 397 TTGGTGAGAGACTGTCAGATTCGATGAGCTGTTGAGTTCTGTCACTGCTACTGCTG 456
 Db 376 TTGGTGAGAGACTGTCAGATTCGATGAGCTGTTGAGTTCTGTCACTGCTACTGCTG 435
 Qy 457 GTTCTGTGCAAGTGTGTGAATCTTAATTAAGCAGACGAGCATGCGCGTAATTGGG 516
 Db 436 GTTCTGTGCAAGTGTGTGAATCTTAATTAAGCAGACGAGCATGCGCGTAATTGGG 495
 Qy 517 CTGGGGGCTGACCAATGCAAGAAAGTCCGAGGATCTGGCTTCTTACGCTAATGATA 576
 Db 496 CTGGGGGCTGACCAATGCAAGAAAGTCCGAGGATCTGGCTTCTTACGCTAATGATA 555
 Qy 577 TCGTCTTGSCATTCGGAAGTCTAAAGTATCACAGAGGGGTGCTGATTAATGACTTG 636
 Db 556 TCGTCTTGSCATTCGGAAGTCTAAAGTATCACAGAGGGGTGCTGATTAATGACTTG 615
 Qy 637 AATTCACCATGATGACGCGGTGGAAGAGAGCTTCTACACAGACGCGGATCATGACTG 696
 Db 616 AATTCACCATGATGACGCGGTGGAAGAGAGCTTCTACACAGACGCGGATCATGACTG 675
 Qy 697 TGTCTTTATTAAGTATGAGAGTACTTCCAGAGAACTGGGGAGCTTAACGGGATACGGGG 756
 Db 676 TGTCTTTATTAAGTATGAGAGTACTTCCAGAGAACTGGGGAGCTTAACGGGATACGGGG 735
 Qy 757 CTGGCAAGACAAAGTATATGCTGTTAATCAACCGCTCGAAGCGGATTTGATGACGAGT 816

| | | | |
|-------------------------------------|--|--|------|
| Db | 736 | CTGGCAAAAGGCAAGTATTATGCTGTAACTACCCGCTCCGAGAGCGGATTGATGACAGT | 795 |
| Qy | 817 | CCATATGAGGCCATTTTCAAGCCGGTCATGTCCAAAGTAAATGAGATGTTCCAGCCTTAGTG | 876 |
| Db | 796 | CCTATGAGGCCATTTTCAAGCCGGTCATGTCCAAAGTAAATGAGATGTTCCAGCCTTAGTG | 855 |
| Qy | 877 | CGGTGTCCTTACAGTGTGGCTCAACCTCCCTATCTCGGGGATCGGTTAGCTTCTTCAATC | 936 |
| Db | 856 | CGGTGTCCTTACAGTGTGGCTCAACCTCCCTATCTCGGGGATCGGTTAGCTTCTTCAATC | 915 |
| Qy | 937 | TATCTATCAAGACACGCCAAGTGTGTGAATTGTCAAGAGCTTTAACTGCTTAGTC | 996 |
| Db | 916 | TAATCTATCAAGACACGCCAAGTGTGTGAATTGTCTCAAGAGCTTTAACTGCTTAGTC | 975 |
| Qy | 997 | TGATGCTGGAGGCGGTGTTACACCAATTCGTAAAGTTTGCCCGGTGCTGACATATAGAGA | 1056 |
| Db | 976 | TGATGCTGGAGGCGGTGTTACACCAATTCGTAAAGTTTGCCCGGTGCTGACATATAGAGA | 1035 |
| Qy | 1057 | CAGCTGTGGCCCTTGATATCGAGAGTCCCTAATGAGCTTCCATATGACTTCCATATGACTTAACTTAAGT | 1116 |
| Db | 1036 | CAGCTGTGGCCCTTGATATCGAGAGTCCCTAATGAGCTTCCATATGACTTCCATTAAGT | 1095 |
| Qy | 1117 | ACTTTGACACAGATTTCAAGCTCCACATCAGTCCCTCCATATGACTTAACAGAACACGA | 1176 |
| Db | 1096 | ACTTTGACACAGATTTCAAGCTCCACATCAGTCCCTCCATATGACTTAACAGAACACGA | 1155 |
| Qy | 1177 | ATGAGTACTGTGAGAGATCAAAACAGCAGCTGTTTGAGAACCTTAGATGCTGCGCAGC | 1236 |
| Db | 1156 | ATGAGTACTGTGAGAGATCAAAACAGCAGCTGTTTGAGAACCTTAGATGCTGCGCAGC | 1215 |
| Qy | 1237 | CACCTGGGGTCCAAACCGAGCGATCTCTGAGAGACGCATCCCTGAGAGAGTGGCGATG | 1296 |
| Db | 1216 | CACCTGGGGTCCAAATGCAAGCGATCTCTGAGAGACGCATCCCTGAGAGAGTGGCGATG | 1275 |
| Qy | 1297 | AGGACGAAGACGACCCCTGACAAAGGCATCTGCATCTGCTCGTGAACAAAGAAATTTGCT | 1356 |
| Db | 1276 | AGGACGAAGACGACCCCTGACAAAGGCATCTGCATCTGCTCGTGAACAAAGAAATTTGCT | 1335 |
| Qy | 1357 | GTTGAGGAAGATTTCTCCGATTTCTGAGAAGAGGAGAGGGGGCCGCAAGAACTTTTCA | 1416 |
| Db | 1336 | GTTGAGGAAGATTTCTCCGATTTCTGAGAAGAGGAGAGGGGGCCGCAAGAACTTTTCA | 1395 |
| Qy | 1417 | ACTTCMAAAAAGCCCAAGAGTCAAAAACAGAGATGAAAAAGAAAAGAACCCAGAGAGA | 1476 |
| Db | 1396 | ACTTCMAAAAAGCCCAAGAGTCAAAAACAGAGATGAAAAAGAAAAGAACCCAGAGAGA | 1455 |
| Qy | 1477 | AGAAAGGAATACCGAAGAGAGAAACCAAGAGAGAACCCAGAACCCAAAGGGGCTCA | 1536 |
| Db | 1456 | AGAAAGGAATACCGAAGAGAGAAACCAAGAGAGAACCCAGAACCCAAAGGGGCTCA | 1515 |
| Qy | 1537 | AGGAGGAGGCCAAGTTGGCTGTAATGACCTCTCCAGCTTGAGCTTCTCTGCTGAGTCCCT | 1596 |
| Db | 1516 | AGGAGGAGGCTCAAGTTGGCTGTAATGACCTCTCCAGCTTGAGCTTCTCTGCTGAGTCCCT | 1575 |
| Qy | 1597 | CACGTTTCTTTCCC 1610 | |
| Db | 1576 | CACGTTTCTTTCCC 1589 | |
| RESULT 5 | | | |
| AAD40884 | | | |
| ID AAD40884 standard; DNA; 2091 BP. | | | |
| AAD40884; | | | |
| XX AC | 30-OCT-2002 (first entry) | | |
| XX DT | | | |
| XX XX | Human histone deacetylase 1 DNA. | | |
| XX DE | | | |
| XX XX | Human; histone deacetylase 1; HDAC1; enzyme; hyperproliferative condition; | | |
| KM | viral infection; prophyllactic; inflammation; phosphorothioate backbone; | | |
| KM | tumour; antileiense; cytostatic; virucide; gene; ds. | | |

| | |
|----------------------------|--|
| XX | Homo sapiens. |
| OS | |
| XX | |
| FH | Key |
| FT | CDS |
| FT | Location/Qualifiers |
| FT | 64..1512 |
| FT | /*tag= A |
| FT | /product= "Human HDA-1 protein" |
| XX | |
| PN | WO200250244-A2. |
| PD | |
| PD | 27-JUN-2002. |
| XX | |
| PE | 07-DEC-2001; 2001WO-US46518. |
| XX | |
| PR | 19-DEC-2000; 2000US-0745167. |
| XX | |
| PA | (ISIS-) ISIS PHARM INC. |
| PI | |
| PI | Monsia BP, Wyatt JR; |
| DR | WPI; 2002-519880/55. |
| P | P-PsDB; AAD40884. |
| XX | |
| PT | Antisense compounds targeted against polynucleotides encoding Histone deacetylase 1 useful for treating hyperproliferative conditions, e.g. cancer of hematopoietic, lymphoid, myeloid or breast, or a viral infection - |
| PS | Example 13; Page 99-102; 120pp; English. |
| CC | The present invention relates to antisense compounds, compositions and methods for modulating the expression of Histone deacetylase 1 (HDAl). |
| CC | Sequences of the invention are useful for inhibiting the expression of HDAl in cells or tissues and for treating an animal having a disease or condition associated with HDAl e.g., hyperproliferative condition, which is cancer of haematopoietic, lymphoid, myeloid or breast or a condition resulting from a viral infection. Antisense compounds either alone or in combination with other antisense compounds or therapeutics can be used as tools in differential and/or combinatorial analyses to elucidate the expression patterns of a portion or the entire complement of genes expressed within cells and tissues. They are commonly used as research reagents and diagnostics. They may also be useful prophylactically such as to prevent or delay infection, inflammation or tumour formation. The present DNA sequence is human HDA-1 DNA. |
| CC | |
| SQ | Sequence 2091 BP; 552 A; 485 C; 544 G; 510 T; 0 other; |
| Query Match | 93.0%; Score 1498; DB 24; Length 2091; |
| Best local similarity | 99.3%; Pred. No. 0; |
| Matches 1504; Conservative | 0; Mismatches 10; Indels 0; Gaps 0; |
| OY | 97 GGGAGCGCAGCAAGATGCGCAGACGCAGGCCACC GGAGAAACTCTGTTACTA CTACG 156 |
| Db | 50 GGGAGCGCAGCAAGATGCGCAGACGCAGGCCACC GGAGAAAGTCTGTTACTA CTACG 109 |
| OY | 157 ACGGGGAATGTTGGAAATTACTATTATGACA CAAGCCCAATGAGGCTCACCGCAATCC 216 |
| Db | 110 ACGGGGAATGTTGGAAATTACTATTATGACA CAAGCCCAATGAGGCTCACCGCAATCC 169 |
| OY | 217 GCATGACTCATTAATTGCTGTCTCAACATACTGTGTCCTACCGAAAAATGAAAATCTATCGCC 276 |
| Db | 170 GCATGACTCATTAATTGCTGTCTCAACATACTGTGTCCTACCGAAAAATGAAAATCTATCGCC 229 |
| OY | 277 CTCACAAAGCCAATGCTGAGAGATGACCAAGTACACAGCGGATGACTTAAATTTCT 336 |
| Db | 230 CTCACAAAGCCAATGCTGAGAGATGACCAAGTACACAGCGGATGACTTAAATTTCT 289 |
| OY | 337 TGCGTCCATCCGCTCCAGATAACATGTGGAGTACAGCAAGCAATGACAGATTCACAG 396 |
| Db | 290 TGCGTCCATCCGCTCCAGATAACATGTGGAGTACAGCAAGCAATGACAGATTCACAG 349 |
| OY | 397 TTGGGAGAGACTGTCAGTATTTCAGTGCGGTTGAGTTCTGTGACTGTGCTACTGGTG 456 |
| Db | |

| | | | |
|----|------|--|------|
| Db | 350 | TTGGTGGAGACATGCCAGTATTCATGGCCCTGTTGAGTTCTGCACTGTCATCTAGT | 409 |
| Qy | 457 | GTTCTGTGGCAAGTGCCTGTGAACCTTAATAAGCAGCAGACGGACATGGCCGTGAATTGGG | 516 |
| Db | 410 | GTTCTGTGGCAAGTGCCTGTGAACCTTAATAAGCAGCAGACGGACATGGCTGTGAATTGGG | 469 |
| Qy | 517 | CTGGGGGCGTCGACCAATGCAAGAAAGATCCAGGACATCGGCTTCGTAGTCAATGATA | 576 |
| Db | 470 | CTGGGGGCGTCGACCAATGCAAGAAAGATCCAGGACATCGGCTTCGTAGTCAATGATA | 529 |
| Qy | 577 | TCGTCCTTGGCCATCCTGGAACTGCTAAAGTATCAACAAGAGGTCGTGAACATTGACATYG | 636 |
| Db | 530 | TCGTCCTTGGCCATCCTGGAACTGCTAAAGTATCAACAAGAGGTCGTGAACATTGACATYG | 589 |
| Qy | 637 | ATATTTACCAATGTGACGGCGCTGAAAGAGCCTTCTACCAACGACCCGGATCATGACTG | 696 |
| Db | 590 | ATATTTACCAATGTGACGGCGCTGAAAGAGCCTTCTACCAACGACCCGGATCATGACTG | 649 |
| Qy | 697 | TGTCCTTTCATAGATGAGAGATACCTTCCAGGAACCTGAGGGACCTACCGGATACCGGGG | 756 |
| Db | 650 | TGTCCTTTCATAGATGAGAGATACCTTCCAGGAACCTGAGGGACCTACCGGATACCGGGG | 709 |
| Qy | 757 | CTGGCAAAAGACAATATATCTGTCTTAACCTACCCGCTCCAGAGCGGGATTGATGACAGT | 816 |
| Db | 710 | CTGGCAAAAGACAATATATCTGTCTTAACCTACCCGCTCCAGAGCGGGATTGATGACAGT | 769 |
| Qy | 817 | CTATATGAGGCCATTTTCACGCCGGTCAATGTCCAAAGTAAATGAGATGTTCCAGCCTATG | 876 |
| Db | 770 | CTATATGAGGCCATTTTCACGCCGGTCAATGTCCAAAGTAAATGAGATGTTCCAGCCTATG | 829 |
| Qy | 877 | CGGATGCTTACATGTGTGCTCAACATCCCATCTGAGGATACGGTTTAGTTAGTTCTTCATC | 936 |
| Db | 830 | CGGATGCTTACATGTGTGCTCAACATCCCATCTGAGGATACGGTTTAGTTAGTTCTTCATC | 889 |
| Qy | 937 | TATCTATCAAAAGACACGCCAAGTGTGGAATTTGTCAAGGCTTTAACTGCTATGTC | 996 |
| Db | 890 | TATCTATCAAAAGACACGCCAAGTGTGGAATTTGTCAAGGCTTTAACTGCTATGTC | 949 |
| Qy | 997 | TGATGCTGGAGGCGGTGTGTTACACATCTGTAAAGTTGCCGGTGTGACATATGAGA | 1056 |
| Db | 950 | TGATGCTGGAGGCGGTGTGTTACACATCTGTAAAGTTGCCGGTGTGACATATGAGA | 1009 |
| Qy | 1057 | CAGCTGTGGCCCTTGATTCGAGATCCCTAATGACTTCCATACATGACTTACTTTGAT | 1116 |
| Db | 1010 | CAGCTGTGGCCCTTGATTCGAGATCCCTAATGACTTCCATACATGACTTACTTTGAT | 1069 |
| Qy | 1117 | ACCTTGGACCAAGTTTCAAGTCCACATCACTCCCTCCAAATATGACTTAAACAGAAACACGA | 1176 |
| Db | 1070 | ACCTTGGACCAAGTTTCAAGTCCACATCACTCCCTCCAAATATGACTTAAACAGAAACACGA | 1129 |
| Qy | 1177 | ATGAGTACTTGGAAAGATCAAAACAGGACCTGTTTGAGAACCTTAAGATGTCGCCGACG | 1236 |
| Db | 1130 | ATGAGTACTTGGAAAGATCAAAACAGGACCTGTTTGAGAACCTTAAGATGTCGCCGACG | 1189 |
| Qy | 1237 | CACCTGGGGTCAAAACGACGGCGATTCTTGAGACGCCATCCTGAGGAGGTGCGCATG | 1296 |
| Db | 1190 | CACCTGGGGTCAAAATGACGGCGATTCTTGAGACGCCATCCTGAGGAGGTGCGCATG | 1249 |
| Qy | 1297 | AGGACGAAAGACACCTTGACAAAGGCGATCTGATCTGCTCTGACAAAGAAATTTGCT | 1356 |
| Db | 1250 | AGGACGAAAGACACCTTGACAAAGGCGATCTGATCTGCTCTGACAAAGAAATTTGCT | 1309 |
| Qy | 1357 | GTCGAGGAAGATTTCTCGATTTCTGAAGAGAGGAGAGGGGGCGCCAGAAATCTTTCCA | 1416 |
| Db | 1310 | GTCGAGGAAGATTTCTCGATTTCTGAAGAGAGGAGAGGGGGCGCCAGAAATCTTTCCA | 1369 |
| Qy | 1417 | ACTTCAAAAAAGCCAGAGAGTCAAAACAGAGATGAAAAAGAAAGAACCCACAGAGAGA | 1476 |
| Db | 1370 | ACTTCAAAAAAGCCAGAGAGTCAAAACAGAGATGAAAAAGAAAGAACCCACAGAGAGA | 1429 |
| Qy | 1477 | AGAAAGGAATCACCGAAGAGAGAAACCAAGAGGAGAAACCCAGAACCCAAAGGGGTCA | 1536 |
| Db | 1430 | AGAAAGGAATCACCGAAGAGAGAAACCAAGAGGAGAAACCCAGAACCCAAAGGGGTCA | 1489 |

| | | | |
|----------|----------|---|------|
| Oy | 1537 | AGAGAGAGGCGCAGTTGGCTGAAATGACCTCTCCACTCTGGCTTCTGATGCTCCT | 1596 |
| Dd | 1490 | AGAGAGAGGTCAAGTTGGCTGAAATGACCTCTCCACTCTGGCTTCTGATGCTCCT | 1549 |
| Oy | 1597 | CACGTTTCTTTTCCC | 1610 |
| Dd | 1550 | CACGTTTCTTCCCC | 1563 |
| RESULT 6 | | | |
| ID | ABK83674 | standard; cDNA; 2091 BP. | |
| XX | AC | ABK83674; | |
| XX | DT | 14-AUG-2002 (first entry) | |
| XX | DE | Human cDNA differentially expressed in granulocytic cells #245. | |
| XX | XX | Human; ss; granulocytic cell; DNA chip; bacterial infection; | |
| KW | KM | viral infection; parasitic infection; protozoal infection; | |
| KW | KM | fungal infection; sterile inflammatory disease; psoriasis; | |
| KW | KM | rheumatoid arthritis; glomerulonephritis; asthma; thrombosis; | |
| KW | KM | cardiac reperfusion injury; renal reperfusion injury; AIDS; | |
| KW | KM | adult respiratory distress syndrome; inflammatory bowel disease; | |
| KW | KM | Crohn's disease; ulcerative colitis; periodontal disease; | |
| KW | KM | granulocyte activation; chronic inflammation; allergy. | |
| OS | XX | Homo sapiens. | |
| XX | PN | MO200228999-A2. | |
| XX | PD | 11-APR-2002. | |
| XX | PF | 03-OCT-2001; 2001WO-US30821. | |
| XX | PR | 03-OCT-2000; 2000US-237189P. | |
| PA | XX | (GENE-) GENE LOGIC INC. | |
| P1 | XX | Beazer-Barclay Y, Weissman SM, Yamaga S, Vockley J; | |
| DR | XX | WPI; 2002-435328/46. | |
| PT | XX | Detecting granulocyte activation by detecting differential expression | |
| PT | XX | of genes associated with granulocyte activation, which serves as | |
| PT | XX | diagnostic markers that is useful for monitoring disease states and | |
| PT | XX | drug toxicity - | |
| PS | XX | Claim 1; SEQ ID No 245; 114pp: English. | |
| XX | XX | The invention relates to detecting (M1) granulocyte (GC) activation | |
| CC | CC | (GCA), by detecting the level of expression of gene(s) (Gs) identified by | |
| CC | CC | DNA chip analysis as given in the specification, and comparing | |
| CC | CC | the expression level to an expression level in an unactivated | |
| CC | CC | GC, where differential expression of Gs is indicative of GCA. | |
| CC | CC | Also included are modulating (M2) GA by contacting GC with an agent | |
| CC | CC | that alters the expression of at least one gene in Gs; (2) screening (M3) | |
| CC | CC | for an agent capable of modulating GCA or an inflammation (especially | |
| CC | CC | chronic) in a tissue, an allergic response in a subject, exposure of a | |
| CC | CC | subject to a pathogen or sterile inflammatory disease using the | |
| CC | CC | gene expression profile; (3) detecting (M4) an inflammation (especially | |
| CC | CC | chronic) in a tissue, an allergic response in a subject, exposure of a | |
| CC | CC | subject to a pathogen or sterile inflammatory disease, by detecting the | |
| CC | CC | level of expression in a sample of the tissue of gene(s) from Gs, where | |
| CC | CC | the level of expression of the gene is indicative of inflammation; | |
| CC | CC | (4) treating (M5) an inflammation (especially chronic) or in a tissue, | |
| CC | CC | an allergic response in a subject, exposure of a subject to a pathogen | |
| CC | CC | or sterile inflammatory disease, by contacting a tissue having | |
| CC | CC | inflammation with an agent that modulates the expression of gene(s) | |
| CC | CC | from Gs in the tissue. M1 is useful for detecting GCA; M2 is useful for | |
| CC | CC | modulating Gs; M3 is useful for screening an agent capable of modulating | |

CC GCM preferably in an inflammation in a tissue; M4 is useful for
CC detecting an inflammation (especially chronic) in a tissue, an allergic
CC response in a subject, exposure of a subject to a pathogen or sterile
CC inflammatory disease (e.g. psoriasis, rheumatoid arthritis,
CC glomerulonephritis, asthma, thrombosis, cardiac reperfusion injury, renal
CC reperfusion injury, ARDS, adult respiratory distress syndrome,
CC inflammatory bowel disease, Crohn's disease, ulcerative colitis,
CC periodontal disease; also bacterial infection, viral infection,
CC parasitic infection, protozoal infection, fungal infection and M5 is
CC useful for treating one of the above conditions. The present
CC sequence represents a gene differentially expressed in granulocytes.
CC Note: The sequence data for this patent did not form part
CC of the printed specification, but was obtained in electronic
CC format directly from MIPD at
CC ftp.wipo.int/pub/published_pat_sequences.

SQ Sequence 2091 BP; 552 A; 485 C; 544 G; 510 T; 0 other;

| | | | | |
|-----------------------|--------------|-------------|---------------|-------------|
| Query Match | 93.0% | Score 1498 | DB 24 | Length 2091 |
| Best Local Similarity | 99.3% | Pred. No. 0 | | |
| Matches 1504 | Conservative | 0 | Mismatches 10 | Indels 0 |
| | | | Gaps | 0 |

| | | | |
|----|-----|--|-----|
| QY | 97 | GGGAGCGCGCAAGATGGCGCAGACGACAGGACCCCGAGGAAAGCTGTGTTACTACG | 156 |
| Db | 50 | GGGAGCGCGCAAGATGGCGCAGACGACAGGACCCCGAGGAAAGCTGTGTTACTACG | 109 |
| QY | 157 | ACGGGAGTGTGGAAATTACTATTATGCAAGAAGCCCAATGAAAGCTTCACCGAATCC | 216 |
| Db | 110 | ACGGGAGTGTGGAAATTACTATTATGCAAGAAGCCCAATGAAAGCTTCACCGAATCC | 169 |
| QY | 217 | GCATGACTCATTAATTTGGCTGCTCAACTATGCTCTCAACGGAAAAATGAAATCTATCGCC | 276 |
| Db | 170 | GCATGACTCATTAATTTGGCTGCTCAACTATGCTCTCAACGGAAAAATGAAATCTATCGCC | 229 |
| QY | 277 | CTCAGAAAGCCAAATGCTGAGAGATGACCAAGTACACAGCGATGACTCATTAATTTCT | 336 |
| Db | 230 | CTCAGAAAGCCAAATGCTGAGAGATGACCAAGTACACAGCGATGACTCATTAATTTCT | 289 |
| QY | 337 | TGCGCTCCATCCGTCGAGTAAACATGTCCGAGTACAGCAAGCAGATGACAGAGATTCAAG | 396 |
| Db | 290 | TGCGCTCCATCCGTCGAGTAAACATGTCCGAGTACAGCAAGCAGATGACAGAGATTCAAG | 349 |
| QY | 397 | TTGGTGAAGACTGTCCAGTATTTCGATGGCTGTTGAGTTCTGTCAGTTGTCTACTGGTG | 456 |
| Db | 350 | TTGGTGAAGACTGTCCAGTATTTCGATGGCTGTTGAGTTCTGTCAGTTGTCTACTGGTG | 409 |
| QY | 457 | GTTCTGTGGCAAGTCTGTGAAACCTTAATTAAGAGAGAGCGACATCGCGCGTGAATTTGG | 516 |
| Db | 410 | GTTCTGTGGCAAGTCTGTGAAACCTTAATTAAGAGAGAGCGACATCGCGCGTGAATTTGG | 469 |
| QY | 517 | CTGGGGGCGCTGCACCATGCAAGAAGTCCGAGGCATCTGGCTTGTGTTACGTCMAATGATA | 576 |
| Db | 470 | CTGGGGGCGCTGCACCATGCAAGAAGTCCGAGGCATCTGGCTTGTGTTACGTCMAATGATA | 529 |
| QY | 577 | TGCTTTGGCCATCTCGAAGCTGCTAAAGTATCACAGAGGGTCTGTACATTGACATTG | 636 |
| Db | 530 | TGCTTTGGCCATCTCGAAGCTGCTAAAGTATCACAGAGGGTCTGTACATTGACATTG | 589 |
| QY | 637 | ATATTACACATGCTGACCGCGGTGGAAGAGGCGCTTACACACACGAGCGGGGTACATGACG | 696 |
| Db | 590 | ATATTACACATGCTGACCGCGGTGGAAGAGGCGCTTACACACACGAGCGGGGTACATGACG | 649 |
| QY | 697 | TGTCCTTTTCATTAAGTATGAGAGAGTACTTCCAGAACTGAGGAGCTACAGGGATACCGGG | 756 |
| Db | 650 | TGTCCTTTTCATTAAGTATGAGAGAGTACTTCCAGAACTGAGGAGCTACAGGGATACCGGG | 709 |
| QY | 757 | CTGGCAAAAGCAAGTATTATGCTGTTAACTACCCGCTCGAGACGGGATTTGATGACGAGT | 816 |
| Db | 710 | CTGGCAAAAGCAAGTATTATGCTGTTAACTACCCGCTCGAGACGGGATTTGATGACGAGT | 769 |
| QY | 817 | CCTATGAGGCCATTTTCAAGCCGGGTACATGCTCCAAAGTATGAGAGTGTTCAGCCCTAAGT | 876 |
| Db | 770 | CCTATGAGGCCATTTTCAAGCCGGGTACATGCTCCAAAGTATGAGAGTGTTCAGCCCTAAGT | 829 |

| | | | |
|----------|-----------|---|------|
| Qy | 877 | CGGCGGCTTTAAACAGTGGGCTCAGACCTCCCTATCTCGGGGATCCGGTAGAGTTGCTTCAATC | 936 |
| Db | 830 | CGGCGGCTTTAAACAGTGGGCTCAGACCTCCCTATCTCGGGGATCCGGTAGAGTTGCTTCAATC | 889 |
| Qy | 937 | TATCTATCAAAAGGACACGCCAAGTGTGGAAATTTGTCAAGAGCTTTTAACTCGCTATGC | 996 |
| Db | 890 | TAACTATCAAAAGGACACGCCAAGTGTGGAAATTTGTCAAGAGCTTTTAACTCGCTATGC | 949 |
| Qy | 997 | TGATGCTGGGAGGCGGTGGTTTACCACTTGTGAACGTTCGCCGTGCTGGACATATAGAG | 1056 |
| Db | 950 | TGAAGCTGGGAGGCGGTGGTTTACCACTTGTGAACGTTCGCCGTGAGGACATATAGAG | 1009 |
| Qy | 1057 | CAGCTGTGGCCCTGGATACGGAAGATCCCTATATGAGCTTCATACATATGACTACTTTGAAT | 1116 |
| Db | 1010 | CAGCTGTGGCCCTGGATACGGAAGATCCCTATATGAGCTTCATACATATGACTACTTTGAAT | 1069 |
| Qy | 1117 | ACTTTGGACCAAGATTTTCAAGCTCCATCACTAGCTCCTTCCAAATATGACTTAACCCAGAACGA | 1176 |
| Db | 1070 | ACTTTGGACCAAGATTTTCAAGCTCCATCACTAGCTCCTTCCAAATATGACTTAACCCAGAACGA | 1129 |
| Qy | 1177 | ATGAGTACCTTGGAGAAATCAAAACAGGACTGTTTGGAAACCTTAGAATCTGCGCGACG | 1256 |
| Db | 1130 | ATGAGTACCTTGGAGAAATCAAAACAGGACTGTTTGGAAACCTTAGAATCTGCGCGACG | 1189 |
| Qy | 1237 | CACCTGGGGGTCCAAACCGCAGGCGAATTCCTGAGACGCGCATCCCTGAGAGAGTGGCGATG | 1296 |
| Db | 1190 | CACCTGGGGGTCCAAATATGACAGGCGAATTCCTGAGACGCGCATCCCTGAGAGAGTGGCGATG | 1249 |
| Qy | 1297 | AGGACGAAGAAGACCCCTGACAAAGCGCATCTGATCTGCTCCTCTTGACAAACGAATTTGCT | 1356 |
| Db | 1250 | AGGACGAAGAAGACCCCTGACAAAGCGCATCTGATCTGCTCCTCTTGACAAACGAATTTGCT | 1309 |
| Qy | 1357 | GTCAGGAAGAGTTCCTCGAATTCGAAAGAGAGAGAGGGGGCGCGAAGACTCTTCCA | 1416 |
| Db | 1310 | GTCAGGAAGAGTTCCTCGAATTCGAAAGAGAGAGAGGGGGCGCGAAGACTCTTCCA | 1369 |
| Qy | 1417 | ACTTCAAAAGGACCAAGAGAGTCAAAAACAGAGATGAAAAAGAGAAAGAACCCAGAGAGAGA | 1476 |
| Db | 1370 | ACTTCAAAAGGACCAAGAGAGTCAAAAACAGAGATGAAAAAGAGAAAGAACCCAGAGAGAGA | 1429 |
| Qy | 1477 | AGAAAGGAATCACCGAAGAGAGAGAAACCAAGAGAGAAAGCCAGAAAGCCAAAGGGGTCA | 1536 |
| Db | 1430 | AGAAAGGAATCACCGAAGAGAGAGAAACCAAGAGAGAAAGCCAGAAAGGGGTCA | 1489 |
| Qy | 1537 | AGGAGAGAGGCAAGTTGGCTGGAATGGAACCTTCACACTCTGAGCTTCTGCTGAGTGCCT | 1596 |
| Db | 1490 | AGGAGAGAGGCAAGTTGGCTGGAATGGAACCTTCACACTCTGAGCTTCTGCTGAGTGCCT | 1549 |
| Qy | 1597 | CACGTTTCTTTTCCC 1610 | |
| Db | 1550 | CACGTTTCTTCCCC 1563 | |
| RESULT 7 | | | |
| ID | AAT12940 | standard; cDNA to mRNA; 2111 BP. | |
| XX | AAT12940; | | |
| XX | AC | AAT12940; | |
| XX | DT | 09-SEP-1996 (first entry) | |
| XX | DE | RPDL transcriptional control protein cDNA. | |
| XX | KM | Transcription; expression; control; diagnosis; study; cancer; | |
| XX | KM | mammary; gastric carcinoma; chromosome 1p34.1; dr. | |
| XX | OS | Homo sapiens. | |
| XX | PH | Key | |
| XX | PT | location/Qualifiers | |
| XX | PT | 64..1512 | |
| XX | CDS | /*Cag= a | |
| XX | FT | /product= RPDL | |
| XX | FT | | |

FT 5'UTR 1..63
 FT /+tag= b
 FT 1513..2111
 FT /+tag= c
 EP08112-A1.
 XX
 PD 24-APR-1996.
 XX
 PF 21-SEP-1995; 95EP-0114884.
 XX
 PR 22-SEP-1994; 94UP-0227876.
 XX
 PA (CANC-) CANCER INST.
 PA (EISA) EISAI CO LTD.
 XX
 PI Furukawa Y, Nakamura Y;
 XX
 DR MPI; 1996-202003/21.
 DR P-PSDB; AAR88919.
 XX
 PT New human transcriptional control protein RPD1 - used to develop
 PT prods. for study and diagnosis involving the protein, partic. for
 PT gene analysis
 PS
 PS Claim 3; Page 10-12; 15pp; English.
 CC AA112940 encodes a transcriptional control protein, RPD1, derived from
 CC a human foetal lung cDNA library. The gene encoding RPD1 is localised
 CC at 1p34.1 on the short arm of chromosome 1, this is a region where a
 CC deletion is recognised in mammary and gastric carcinomas. The RPD1
 CC gene is an important gene and has been found to be expressed in all
 CC the following human tissues: heart, kidney, liver, lung, pancreas,
 CC placenta, skeletal muscle, large intestine, peripheral leukocyte,
 CC ovary, prostate, small intestine, spleen, testis and thymus gland;
 CC but is not present in brain tissue. RPD1 cDNA exhibits homology with
 CC the yeast transcription factor RPD3 and is believed to have a similar
 CC function. RPD1 and DNA encoding it can be used in studying the
 CC interactions of the protein with DNA and other proteins in the cell.
 CC
 XX
 XX Sequence 2111 BP; 572 A; 485 C; 544 G; 510 T; 0 other;
 SQ
 Query Match 93.0%; Score 1498; DB 17; Length 2111;
 Best Local Similarity 99.3%; Pred. No. 0;
 Matches 1504; Conservative 0; Mismatches 10; Indels 0; Gaps 0;
 QY 97 GGGAGCGAGCAAGATGCGCAGACGCGAGGCAACCGAGAGAAAGTCTGTACTACTACG 156
 DB 50 GGGAGCGAGCAAGATGCGCAGACGCGAGGCAACCGAGAGAAAGTCTGTACTACTACG 109
 QY 157 ACGGGAGTGTGGAATTAATTAATTAATGAAGGCCCAATGAAGCTTCAACCGAATCC 216
 DB 110 ACGGGAGTGTGGAATTAATTAATTAATGAAGGCCCAATGAAGCTTCAACCGAATCC 169
 QY 217 GCATGACTCAATATTGCTGCTCACTATGCTCTCTACCGAAAAATGGAATCTATCGCC 276
 DB 170 GCATGACTCAATATTGCTGCTCACTATGCTCTCTACCGAAAAATGGAATCTATCGCC 229
 QY 277 CTCACAAAGCAATGCTGAGAGATGACCAAGTACCAAGCGATGACTACATTAATTTCT 336
 DB 230 CTCACAAAGCAATGCTGAGAGATGACCAAGTACCAAGCGATGACTACATTAATTTCT 289
 QY 337 TGGGCTTCATCCGTCAGATTAACATGTCGAGATACAGCAAGCGATGACAGATTCAACG 336
 DB 290 TGGGCTTCATCCGTCAGATTAACATGTCGAGATACAGCAAGCGATGACAGATTCAACG 349
 QY 397 TTGGTAGAGACTGTCAATGATGAGTCTGTTTGAATTTCTGTCAAGTTTCTACTAGTG 456
 DB 350 TTGGTAGAGACTGTCAATGATGAGTCTGTTTGAATTTCTGTCAAGTTTCTACTAGTG 409
 QY 457 GTTCTGTGGCAAGTGTGTGAAAATTATTAAGACGACGACGACATGCGCGTAATTGGG 516
 DB 410 GTTCTGTGGCAAGTGTGTGAAAATTATTAAGACGACGACGACATGCGCGTAATTGGG 469

QY 517 CTGGGGGCTTGACCAATGCAAGAAAGTCCAGAGCATCTGCTTGTGTAAGTATGATA 576
 DB 470 CTGGGGGCTTGACCAATGCAAGAAAGTCCAGAGCATCTGCTTGTGTAAGTATGATA 529
 QY 577 TCGTCTTGCCATCTCTGGAACCTGTAAAGTATCACCAGAGGCTGTGATCAATTGACATTG 636
 DB 530 TCGTCTTGCCATCTCTGGAACCTGTAAAGTATCACCAGAGGCTGTGATCAATTGACATTG 589
 QY 637 AATATCAACCATGATGACCGGCTGGAAGAGGCGCTTGTACACCGAGCGGGATGACTG 696
 DB 590 AATATCAACCATGATGACCGGCTGGAAGAGGCGCTTGTACACCGAGCGGGATGACTG 649
 QY 697 TGTCTTTTATTAAGTATGAGAGTACTTCCAGAACTGGGAGCTTAACGGGATACCGGAG 756
 DB 650 TGTCTTTTATTAAGTATGAGAGTACTTCCAGAACTGGGAGCTTAACGGGATACCGGAG 709
 QY 757 CTGGCAAGACAAAGTATTAATGCTGTTAACTACCCGCTCCGAGACGGGATTTGATGACAGT 816
 DB 710 CTGGCAAGACAAAGTATTAATGCTGTTAACTACCCGCTCCGAGACGGGATTTGATGACAGT 769
 QY 817 CCTATGAGGCCATTTTCAAGCCGGTCAATGCTCCAAAGTATGAGAGTTCACGCCATAGG 876
 DB 770 CCTATGAGGCCATTTTCAAGCCGGTCAATGCTCCAAAGTATGAGAGTTCACGCCATAGG 829
 QY 877 CGGTGCTTTAAGTATGAGTCTGAGACTCCCTATCTGGGAGTGGTTAGGTTGCTTCAATC 936
 DB 830 CGGTGCTTTAAGTATGAGTCTGAGACTCCCTATCTGGGAGTGGTTAGGTTGCTTCAATC 889
 QY 937 TATCTATCAAGAGACACGCGCAAGTGTGGAATTTGTCAAGAGCTTTAACTCTGCTATGC 996
 DB 890 TATCTATCAAGAGACACGCGCAAGTGTGGAATTTGTCAAGAGCTTTAACTCTGCTATGC 949
 QY 997 TGAATGTGGAGAGCGGTGTGTTACCATTCGTAAGCTTCCGCTGCTGACATATGAGA 1056
 DB 950 TGAATGTGGAGAGCGGTGTGTTACCATTCGTAAGCTTCCGCTGCTGACATATGAGA 1009
 QY 1057 CAGCTGTGCGCTTGATAGGAGATCCCTAATGAGCTTCAATGACTACTTTGAAT 1116
 DB 1010 CAGCTGTGCGCTTGATAGGAGATCCCTAATGAGCTTCAATGACTACTTTGAAT 1069
 QY 1117 ACTTTGACCAAGATTTCAAGCTCCACATGATCTTTCAAATATGACTAAACGAACGAA 1176
 DB 1070 ACTTTGACCAAGATTTCAAGCTCCACATGATCTTTCAAATATGACTAAACGAACGAA 1129
 QY 1177 ATGAGTACTGTGAGAAAGATCAAAACGCGACTGTTTGAAGACCTTGAAGTCTGCCAGG 1236
 DB 1130 ATGAGTACTGTGAGAAAGATCAAAACGCGACTGTTTGAAGACCTTGAAGTCTGCCAGG 1189
 QY 1237 CACCTGGGGTCCAAACGCGAGGGATTCCTGAGGAGCGCATCCCTGAGGAGAGTGGCGATG 1296
 DB 1190 CACCTGGGGTCCAAACGCGAGGGATTCCTGAGGAGCGCATCCCTGAGGAGAGTGGCGATG 1249
 QY 1297 AGGACGAGACGACCTCTGCAAGCGCATGTGATCTGCTCTGTGAACGAATTTGCTT 1356
 DB 1250 AGGACGAGACGACCTCTGCAAGCGCATGTGATCTGCTCTGTGAACGAATTTGCTT 1309
 QY 1357 GTGAGGAAGAGTTCTTCGATTTCTGAAGAGAGGAGAGGGGGCCGCAAGAACTTTTCCA 1416
 DB 1310 GTGAGGAAGAGTTCTTCGATTTCTGAAGAGAGGAGAGGGGGCCGCAAGAACTTTTCCA 1369
 QY 1417 ACTTCAAAAAGCGCAAGAGTCAAAACAGAGGATGAAAAAGGAAAGCCCGAGAGAG 1476
 DB 1370 ACTTCAAAAAGCGCAAGAGTCAAAACAGAGGATGAAAAAGGAAAGCCCGAGAGAG 1429
 QY 1477 AGAAAGAAATCAACCGAAGAGAGAAAAACCAAGAGAGAGACCAAGAGCGGCTCA 1536
 DB 1430 AGAAAGAAATCAACCGAAGAGAGAAAAACCAAGAGAGAGACCAAGAGCGGCTCA 1489
 QY 1537 AGAGAGAGCGCAAGTTGGCTGATATGACCTCTCCAGCTCTGGCTTCTGCTGAAGTCCCT 1596
 DB 1490 AGAGAGAGCGCAAGTTGGCTGATATGACCTCTCCAGCTCTGGCTTCTGCTGAAGTCCCT 1549

QY 1597 CACGTTTCTTCCC 1610
1550 CACGTTTCTTCCC 1563
RESULT 8
ID ABS58329 standard; DNA; 1671 BP.
XX ABS58329;
AC ABS58329;
XX 04-MAR-2003 (first entry)
XX DNA encoding TAT-dMtc-HDAC1 fusion protein.
XX HIV; human immunodeficiency virus; Tat; HIV Tat inhibitor; virus;
XX HIV transcription; AIDS; acquired immunodeficiency syndrome;
XX TAT-dMtc-HDAC1; gene; ds; human.
XX Chimeric - Human immunodeficiency virus type 1.
OS Chimeric - Homo sapiens.
OS Synthetic.
XX Key Location/Qualifiers
FH CDS 1..1671
FT /*tag= a
FT /product= "TAT-dMtc-HDAC1 fusion protein"
XX WO200285948-A1.
XX 31-OCT-2002.
XX 19-APR-2002; 2002WO-KR00730.
XX 20-APR-2001; 2001KR-0021449.
XX 18-APR-2002; 2002KR-0021307.
XX (HURM/) HUR M.
XX HUR M, Chong DL;
XX WPI; 2003-093103/08.
XX P-PSDB; ABG72562.
XX
XX New fusion proteins, useful for repressing HIV transcription regulating
PT expression of AIDS viral RNA to inhibit the proliferation of virus and
PT production of resistant virus
XX
XX Claim 5; Page 55-57; 60pp; English.
XX
XX This invention relates to a novel fusion protein which may be used to
XX repress human immunodeficiency virus (HIV) transcription. The protein
XX comprises a transcription inhibitory polypeptide or its compound and a
XX polypeptide or its compound which recognizes the RNA strand around
XX expression control regions or viral long terminal repeat (LTR) promoter
XX cis-acting elements. The fusion proteins of the invention may have Anti
XX -HIV activity and may be used as an inhibitor of HIV Tat. The fusion
XX proteins of the invention are useful for repressing HIV transcription
XX regulating expression of AIDS viral RNA to inhibit the proliferation of
XX virus and production of resistant virus. The method of repressing HIV
XX transcription is useful for treating AIDS. The present sequence
XX represents the DNA sequence encoding the TAT-dMtc-HDAC1 fusion protein of
XX the invention.
XX
SQ Sequence 1671 BP; 471 A; 386 C; 443 G; 371 T; 0 other;
Query Match 89.1%; Score 1436.2; DB 25; Length 1671;
Best Local Similarity 99.4%; Pred. No. 0;
Matches 1441; Conservative 0; Mismatches 8; Indels 0; Gaps 0;
QY 111 ATGCGCGAGACGACGCGCGCGAGAAAGTCTGTACTACTACGACGCGGAGTGTGGA 170
Db 223 ATGCGCGAGACGACGCGCGCGAGAAAGTCTGTACTACTACGACGCGGAGTGTGGA 282

QY 171 AATTACTATTATGACAGGCGACCAATGAAGCTTACCGAATCCGATGACTCATAT 230
Db 283 AATTACTATTATGACAGGCGACCAATGAAGCTTACCGAATCCGATGACTCATAT 342
QY 231 TTGCTGCTCACTATGCTCTTACCGAAAAATGGAATCTATGCGCTCAAAAGCCAT 290
Db 343 TTGCTGCTCACTATGCTCTTACCGAAAAATGGAATCTATGCGCTCAAAAGCCAT 402
QY 291 GCTGAGAGATGACCAAGTACCAAGGATGATGATCACTTAATTTCTGCGCTCATCGT 350
Db 403 GCTGAGAGATGACCAAGTACCAAGGATGATGATCACTTAATTTCTGCGCTCATCGT 462
QY 351 CCAGATTAACATGTCGAGATACAGCAAGCAGATGACAGATTCACGTTGAGAGACTGT 410
Db 463 CCAGATTAACATGTCGAGATACAGCAAGCAGATGACAGATTCACGTTGAGAGACTGT 522
QY 411 CCAGATTAACATGTCGAGATGATGATGATGATGATGATGATGATGATGATGATG 470
Db 523 CCAGATTAACATGTCGAGATGATGATGATGATGATGATGATGATGATGATGATG 582
QY 471 GCTGTAATCTTAATTAAGACGACGAGGATGATGATGATGATGATGATGATGATGAT 530
Db 583 GCTGTAATCTTAATTAAGACGACGAGGATGATGATGATGATGATGATGATGATGAT 642
QY 531 CATGCAAAAGAGTCCGAGGATGATGATGATGATGATGATGATGATGATGATGATG 590
Db 643 CATGCAAAAGAGTCCGAGGATGATGATGATGATGATGATGATGATGATGATGATG 702
QY 591 CTGGAATCTGTAAGATACACGAGGATGATGATGATGATGATGATGATGATGATGAT 650
Db 703 CTGGAATCTGTAAGATACACGAGGATGATGATGATGATGATGATGATGATGATGAT 762
QY 651 GACGGGCTGGAAGAGGCTTCTACACGAGGATGATGATGATGATGATGATGATGATGAT 710
Db 763 GACGGGCTGGAAGAGGCTTCTACACGAGGATGATGATGATGATGATGATGATGATGAT 822
QY 711 TATGAGAGTACTCTCCAGAGATGAGGATGATGATGATGATGATGATGATGATGATG 770
Db 823 TATGAGAGTACTCTCCAGAGATGAGGATGATGATGATGATGATGATGATGATGATG 882
QY 771 TATGAGTCTGTTAATCACTCCGCTCCGAGGATGATGATGATGATGATGATGATGAT 830
Db 883 TATGAGTCTGTTAATCACTCCGCTCCGAGGATGATGATGATGATGATGATGATGATG 942
QY 831 TTGAAGCCGCTATGTCGAAAGTATGAGATGTCGAGCTGATGAGGATGATGATGATG 890
Db 943 TTGAAGCCGCTATGTCGAAAGTATGAGATGTCGAGCTGATGAGGATGATGATGATG 1002
QY 891 TGTGCTCAGACTCCCTATCTGAGGATGAGGATGATGATGATGATGATGATGATGATG 950
Db 1003 TGTGCTCAGACTCCCTATCTGAGGATGAGGATGATGATGATGATGATGATGATGATG 1062
QY 951 CAGGCCAAGTGTGGAATTTGTCGAGGATTTAAGCTTCTGATGATGATGATGATGATG 1010
Db 1063 CAGGCCAAGTGTGGAATTTGTCGAGGATTTAAGCTTCTGATGATGATGATGATGATG 1122
QY 1011 GGTGTTAAGCACTGTTGATGATGATGATGATGATGATGATGATGATGATGATGATG 1070
Db 1123 GGTGTTAAGCACTGTTGATGATGATGATGATGATGATGATGATGATGATGATGATG 1182
QY 1071 GATACGAGATCCCTATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1130
Db 1183 GATACGAGATCCCTATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1242
QY 1131 TTGAAGTCAATCACTGATGATGATGATGATGATGATGATGATGATGATGATGATG 1190
Db 1243 TTGAAGTCAATCACTGATGATGATGATGATGATGATGATGATGATGATGATGATG 1302
QY 1191 AAGATCAAAAGGAGCTGTTGAGAACTTGAAGTGTGCGGACGACCTGCGGATGATG 1250
Db 1303 AAGATCAAAAGGAGCTGTTGAGAACTTGAAGTGTGCGGACGACCTGCGGATGATG 1362


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Db      481 CTGGAACCTGTAAGATACACGAGGGGTCGTATGACATTGACATTTGATCCATCGT 540
Qy      651 GACGGGTGGAGAGGCTCTCTACACGACCGGGTCATGATGTCCTTCAATAG 710
Db      541 GACGGGTGGAGAGGCTCTCTACACGACCGGGTCATGATGTCCTTCAATAG 600
Qy      711 TATGAGAGTACTTCCAGAGAACTGGGACCTACGAGATACCGGGCTGGCAAAACAAG 770
Db      601 TATGAGAGTACTTCCAGAGAACTGGGACCTACGAGATACCGGGCTGGCAAAACAAG 660
Qy      771 TATTATGCTGTAACTAACCCGCTCCGAGAGAGGATTTGATACAGAGTCCTATGAGCCATT 830
Db      661 TATTATGCTGTAACTAACCCGCTCCGAGAGAGGATTTGATACAGAGTCCTATGAGCCATT 720
Qy      831 TTCAGCCCGGTCAATGCTCAAAAGTAAATGAGATTTCCAGAGCTAGTCCGGTGGCTTACAG 890
Db      721 TTCAGCCCGGTCAATGCTCAAAAGTAAATGAGATTTCCAGAGCTAGTCCGGTGGCTTACAG 780
Qy      891 TGTGGCTCAGACTCCCTATCTGGGGATCGGTTAGGTTGCTTCAATCTATCTATCAAAAGA 950
Db      781 TGTGGCTCAGACTCCCTATCTGGGGATCGGTTAGGTTGCTTCAATCTATCTATCAAAAGA 840
Qy      951 CAGGCCAAGTGTGGAATTTGTCACAGAGCTTTAACTGCTATGCTGATGCTGGAGGC 1010
Db      841 CAGGCCAAGTGTGGAATTTGTCACAGAGCTTTAACTGCTATGCTGATGCTGGAGGC 900
Qy      1011 GGTGGTTACACATTCGTAACTGTCGCGGTCGAGCATATGACAGCTGTCGCGCTG 1070
Db      901 GGTGGTTACACATTCGTAACTGTCGCGGTCGAGCATATGACAGCTGTCGCGCTG 960
Qy      1071 GATACGAGATCCCTATGATGATGCTTCAATCAATGACTACTTTGAAATCTTTGAGCAGAT 1130
Db      961 GATACGAGATCCCTATGATGATGCTTCAATCAATGACTACTTTGAAATCTTTGAGCAGAT 1020
Qy      1131 TTCAAGCTCAATCAGTCTCTTCAATATGACTTAACTCAAGAACAGATGATGATGAG 1190
Db      1021 TTCAAGCTCAATCAGTCTCTTCAATATGACTTAACTCAAGAACAGATGATGATGAG 1080
Qy      1191 AAGATCAACAGGAGCTGTTGAGAACCTTGAAGTGTGCGGACGACCTGGGGTCCAA 1250
Db      1081 AAGATCAACAGGAGCTGTTGAGAACCTTGAAGTGTGCGGACGACCTGGGGTCCAA 1140
Qy      1251 ACCGAGCGCATCTCTGAGAGAGCCATCCCTGAGAGAGTGGCGATGAGACGAGACGAC 1310
Db      1141 ATCGAGCGCATCTCTGAGAGAGCCATCCCTGAGAGAGTGGCGATGAGACGAGACGAC 1200
Qy      1311 CTGACAGCGCATCTCTGATCTGCTCTGACAAAGAAATTCCTGTGAGAAAGTTTC 1370
Db      1201 CTGACAGCGCATCTCTGATCTGCTCTGACAAAGAAATTCCTGTGAGAAAGTTTC 1260
Qy      1371 TCCGATTTGAAAGAGAGAGAGGGGGCGCAAGAACTCTTCCAACTTCAAAAAAGCC 1430
Db      1261 TCCGATTTGAAAGAGAGAGAGGGGGCGCAAGAACTCTTCCAACTTCAAAAAAGCC 1320
Qy      1431 AAGAGATCAAAACAGAGATGAAAAAGAAAAAGAACCCAGAGAGAAAGAAAGATCAC 1490
Db      1321 AAGAGATCAAAACAGAGATGAAAAAGAAAAAGAACCCAGAGAGAAAGAAAGATCAC 1380
Qy      1491 GAAAGAGAGAAAAACAAGAGAGAAAGAACCCAAAGGGGTCAAGAGAGAGCCCAAG 1550
Db      1381 GAAAGAGAGAAAAACAAGAGAGAAAGAACCCAAAGGGGTCAAGAGAGAGCCCAAG 1440
Qy      1551 TTGGCTGAT 1561
Db      1441 TTGGCTGAT 1451

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RESULT 11
AAS81302
ID AAS81302 standard; cDNA; 1582 BP.
XX AC AAS81302;
XX

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Dt      13-FEB-2002 (first entry)
Xx      DNA encoding novel human diagnostic protein #17106.
Xx      Human; chromosome mapping; gene mapping; gene therapy; forensic;
Xx      food supplement; medical imaging; diagnostic; genetic disorder; ss.
Xx      Homo sapiens.
Xx      MO200175067-A2.
Xx      11-OCT-2001.
Xx      30-MAR-2001; 2001WO-US08631.
Xx      31-MAR-2000; 2000US-0540217.
Xx      23-AUG-2000; 2000US-0649167.
Xx      (HYSE-) HYSBQ INC.
Xx      Dermanac RT, Liu C, Tang YT;
Xx      WPI; 2001-639362/73.
Xx      P-PSDB; ABG17115.
Xx      New isolated polynucleotide and encoded polypeptides, useful in
Xx      diagnostics, forensic, gene mapping, identification of mutations
Xx      responsible for genetic disorders or other traits and to assess
Xx      biodiversity -
Xx      Claim 1, SEQ ID No 17106; 103pp; English.
Xx      The invention relates to isolated polynucleotide (I) and
Xx      polypeptide (II) sequences. (I) is useful as hybridisation probes,
Xx      polymerase chain reaction (PCR) primers, oligomers, and for chromosome
Xx      and gene mapping, and in recombinant production of (II). The
Xx      polynucleotides are also used in diagnostics as expressed sequence tags
Xx      for identifying expressed genes. (I) is useful in gene therapy techniques
Xx      to restore normal activity of (II) or to treat disease states involving
Xx      (II). (II) is useful for generating antibodies against it, detecting or
Xx      quantitating a polypeptide in tissue, as molecular weight markers and as
Xx      a food supplement. (II) and its binding partners are useful in medical
Xx      imaging of sites expressing (II). (I) and (II) are useful for treating
Xx      disorders involving aberrant protein expression or biological activity.
Xx      The polypeptide and polynucleotide sequences have applications in
Xx      diagnostics, forensics, gene mapping, identification of mutations
Xx      responsible for genetic disorders or other traits to assess biodiversity
Xx      and to produce other types of data and products dependent on DNA and
Xx      amino acid sequences. AAS64197-AAS94564 represent novel human
Xx      diagnostic coding sequences of the invention.
Xx      Note: The sequence data for this patent did not appear in the printed
Xx      specification, but was obtained in electronic format directly from WIPO
Xx      at ftp.wipo.int/pub/published_pat_sequences.
Xx      Sequence 1582 BP; 422 A; 376 C; 441 G; 343 T; 0 other;
Xx
Qy      Query Match      85.5%; Score 1378; DB 23; Length 1582;
Xx      Best Local Similarity 96.5%; Pred. No. 0;
Xx      Matches 1475; Conservative 0; Mismatches 40; Indels 13; Gaps 6;
Xx
Qy      97 GGGAGCGAGCAAGATGAGCGCAGACGACGAGCAACCGGAGAGAAAGTCTGTTACTACG 156
Xx      |||||
Xx      55 GGGAGCGAGCAAGATGAGCGCAGACGACGAGCAACCGGAGAGAAAGTCTGTTACTACG 114
Xx      |||||
Qy      157 ACGGGAGTGTGAAATTAATAATTATGAC-AAAGCCACCAATGAGAGCTC-ACCGAAT 214
Xx      |||||
Xx      115 ACGGGAGTGTGAAATTAATAATTATGAGAGAGGAGCAACCAATGAGAGCTCAGACGAAT 174
Xx      |||||
Qy      215 CCGCATGACTCAATAATTTGCTGCTCAATATGTCCTTACGAAAAATGAAATCTATG 274
Xx      |||||
Xx      175 CCGCATGACTCAATAATTTGCTGCTCAATATGTCCTTACGAAAAATGAAATCTATG 234
Xx      |||||
Qy      275 CCTCACAAAGCAATGTGAGAGATGACCAAGTACACAGAGATGACTATTAATT 334

```


Query Match 50.8%; Score 818; DB 24; Length 1997;
 Best Local Similarity 73.4%; Pred. No. 4,4e-238;
 Matches 1046; Conservative 0; Mismatches 380; Indels 0; Gaps 0;

QY 126 GGCACCCGAGGAAAGCTCTTACTACTAGACGGGGATGTGGAAATTAATCTATTATGGA 185
 DB 187 GGGGGAGAGAAAGTGTCTACTACTAGATGGTATATTTGGCAATTAATTTATGGC 246
 QY 186 CAAGGCGACCAATGAAAGCTCAACCGATGATGATATTAATTTGCTGCTCACTAT 245
 DB 247 CAGGGTCATCCATGAGGCTCATAGATCCGATGATCATTAATCTTGCTGCTAAATTA 306
 QY 246 GGTCTACCGAAAAATGAAATCTATCGCCCTCAACAAGCCAATGCTGAGAGATGCC 305
 DB 307 GGTTTATACGAAAAATGAAATATATAGGCTCATTAAGCCATGCTGTGAAGAAATGACT 366
 QY 306 AAGTACCAAGCGATGATCAATTAATTTGGGCTCCATCCGTCAGATTAATGCTG 365
 DB 367 AATATCCACAGCGATGATATCAAGTTTCTACGATCAATTAAGACCAATTAATGCTCT 426
 QY 366 GAGTACGAGAGAGATGAGATTCAGTTGGTGAAGACTGTCAGATTCAGATGCG 425
 DB 427 GAGTACGATGAGAGATGAGATTTAAGTGGAGAGATTTGCGGTGTTGATGGA 486
 QY 426 CTGTTGAGTTCTGTCAAGTTGTCTACTGTGTCTGTGCGCAAGTGTGTAATCTTAAT 485
 DB 487 CTCTTGAGTTTGTCAAGCTCTCAAGGGTGTTCAGTTGCTGGGGGTGTGAATTAAC 546
 QY 486 AAGGAGAGAGAGATGCGCGTGAATTTGGGCTGGGGGCTGCAACATGCAAGAAAGTCC 545
 DB 547 CGGCAACAACTGATATGCTGTCATATGGGCTGAGAGATCAATATCAATGCAAGAAAGTCA 606
 QY 546 GAGGCAATCTGGCTTCTGTGTCATATGATATGCTGTGGCAATCCCGGAACTGCTAAG 605
 DB 607 GAGGCAATCAGGGTTCGTCTATATGATATGATATGCTGTCCATCTCGAATTAATCTTAAG 666
 QY 606 TATCACCAGAGGGTGTCTGATCATTTGATGATGATTAATTCACATGATGAGCGGCTGAAG 665
 DB 667 TATCATCAGAGATCTTATATATTTGACATAGACATCAACATGATGATGTTGAGGAA 726
 QY 666 GGCCTTCAACCAAGGACCGGGTCAATGATGATGCTGCTCTTCAATAGATGAGATCTTC 725
 DB 727 GCTTTTATCAACAAGATCCGATGATGACGCTCATTCATTAATTAATGAGGATTAATCTT 786
 QY 726 CAGAGAACTGGGACCTCAAGGATACCGGGCTGGCAAGCAATTTATGCTGTTAAC 785
 DB 787 CCTGGAACAGAGACTTGAAGGATATGCTGAGAAAGGAAATTAATGCTGTCAT 846
 QY 786 TACCCGCTCGAGACGGGATTTGATGACGATGATGATGATGATGATGATGATGATGATG 845
 DB 847 TTTCCCATGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 906
 QY 846 TCCAAAGTATGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 905
 DB 907 TCAAAAGTATGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 966
 QY 906 CTATCTGGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 965
 DB 967 CTGCTGGGAGACGGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1026
 QY 966 GAATTTGTCAAGAGCTTAACTGCTGATGATGATGATGATGATGATGATGATGATGATG 1025
 DB 1027 GAAGTACGAAACTTTTAACTGCTGATGATGATGATGATGATGATGATGATGATGATGATG 1086
 QY 1026 CGTAAAGTTCGCGGTGCTGAGATATGAGACAGCTGTCCTGATGATGATGATGATGATG 1085
 DB 1087 CGGAATGTCGCGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1146
 QY 1086 AATGAGCTTCATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1145
 DB 1147 AATGAGTTCATATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1206
 QY 1146 AGTCTTCAATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1205

DB 1207 AGTCTTCAAAATGATGAAACCAAGACCTCCAGATATATGAAAAAGATTAACAGCGT 1266
 QY 1206 CTGTTGAGAACCTTGAATGTCGCGGACGACGACCTGGGGTCCAAACGAGCGATTCCT 1265
 DB 1267 TTTATTTGAAATCTACGATATGTTTCCATGCAATGCACTGGTGTTCAAATGCAAGCTATTCCA 1326
 QY 1266 GAGGACCGCATCCCTGAGAGAGATGCGATGAGAGACGAAGACGACCTGACAAAGCCATC 1325
 DB 1327 GAGGATGCTGTTCAATGAAACAGTGGATGAGATGAGAGAGAGAGAGAGAGAGAGAGAGAT 1386
 QY 1326 TCGATCTGCTCTTGACAAACGATGCTGATGAGAGAGAGATGCTCCGATTTGAAAG 1385
 DB 1387 TCCATTCGAGATCAAGACAAAGGATGCTGATGAGAGAGAGATTTCAATTCGAGAT 1446
 QY 1386 GAGGAG 1445
 DB 1447 GAAAGTGAAGAGAGTGTGAGAAATGTTGCTGATCAATGAAGAGAGAGAGAGAGAGAGAG 1506
 QY 1446 GAGGATGAAAG 1505
 DB 1507 ATTTAG 1566
 QY 1506 AAGGAG 1551
 DB 1567 TCCAGAGCAATATGATGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1612

RESULT 13
 AA232066
 ID AA232066 standard; DNA; 1985 BP.
 XX
 AC AA232066;
 XX
 DT 10-JAN-2000 (first entry)
 XX
 DE Human METH2 related EST U31814.
 XX
 KW Human; METH1; METH2; anti-angiogenic; metalloprotease thrombospondin;
 KW cancer; diagnosis; hyperproliferative disorder; autoimmune disease;
 KW angiogenesis inhibitor; abnormal wound healing; inflammation;
 KW rheumatoid arthritis; psoriasis; endometrial bleeding disorder;
 KW diabetic retinopathy; macula degeneration; haemangioma; detection;
 KW arterial-venous malformation; immune deficiency; ss.
 XX
 OS Homo sapiens.
 XX
 PN MO9937660-A1.
 XX
 PD 29-JUL-1999.
 XX
 PF 22-JAN-1999; 99MO-US01313.
 XX
 PR 23-JAN-1998; 98US-0072298.
 PR 28-AUG-1998; 98US-0098539.
 XX
 PA (TRUE/) IRUELA-ARISPE L.
 PA (HAST/) HASTINGS G A.
 PA (RUBE/) RUBEN S M.
 XX
 PI Iruele-Arispe L, Hastings GA, Ruben SM;
 XX
 DR WPI; 1999-590684/50.
 XX
 PT New isolated metalloprotease thrombospondin polypeptides, useful for
 PT treating hyperproliferative disorders, cancers or autoimmune disorders
 PT
 PS Disclosure; Page 444-446; 457pp; English.
 XX
 CC AA232000 and AA232001 encode, and AAY49501 and AAY49502 represent, human
 CC metalloprotease thrombospondin (METH) proteins METH1 and METH2
 CC respectively. METH1 and METH2 have been found to be potent inhibitors of

CC angiogenesis both in vitro and in vivo. They can be used for treating
CC cancer and other disorders related to angiogenesis including abnormal
CC wound healing, inflammation, rheumatoid arthritis, psoriasis,
CC endometrial bleeding disorders, diabetic retinopathy, some forms of
CC macula degeneration, haemangiomas, and arterial-venous malformations.
CC They may be useful in treating deficiencies or disorders of the immune
CC system, by activating or inhibiting the proliferation, differentiation,
CC or mobilisation (chemotaxis) of immune cells. The etiology of these
CC immune deficiencies or disorders may be genetic, somatic, such as
CC cancer or some autoimmune disorders, acquired (e.g. by chemotherapy or
CC toxins), or infectious. They can also be used to treat inflammatory or
CC conditions, both chronic and acute conditions. The products can also be
CC used for detection and diagnosis. AA32002 to AA32080, and AA49503 to
CC AA49511 represent sequences given in the exemplification of the present
CC invention.

XX Sequence 1985 BP, 626 A, 360 C, 454 G, 545 T, 0 other;

Query Match 50.0%; Score 805.2; DB 20; Length 1985;
Best Local Similarity 72.8%; Pred. No. 3.5e-234;
Matches 1038; Conservative 0; Mismatches 388; Indels 0; Gaps 0;

```
QY 126 GGCACCCGAGAGAAAGTCTGTTACTACTACGAGCGGAGTGTGGAAATTAATTATGGA 185
DB 223 GCGCGCAAAAAAAGTCTGCTACTACTACGAGCGGTGATTTGGAAATTAATTATGGA 282
QY 186 CAAGGCCAACCAATGAAGCTCAACCGAATCCGCAATCACTAATTTGCTGCTCAACTAT 245
DB 283 CAGGCTCAATCCATGAAGCTCATAGAAATCCGAGAGCCCAATTAATTTGCTTTAAATAT 342
QY 246 GGTCTCAACCAAAATGGAATCTATCGCCCTCAAAAGCCAAATGCTGAGAGATGACC 305
DB 343 GGCCTATACAGAAAAATGGAATATATAGGCCCAATAAAGCACTGCCGAGAAATGACA 402
QY 306 AAGTACACAGCGATGACTAATTAATTTCTGGCTCACTCCGTCAGATTAATGTCG 365
DB 403 AAATATCAAGTGTATGATATATCAAAATTTCTACGCTCAATTAAGACGATTAATCATGCT 462
QY 366 GAGTACAGCAAGATGATGAGAAATTCAGTGGTGAGACGTGCCGATTTGATGAGGC 425
DB 463 GAGTATATGAGAGATGATCAATATTTATGTTGAGAAATTTGCCAGCTTTGATGAGA 522
QY 426 CTGTTTGAGTTCTGCACTTGTCTACTGCTGTTCTGTGCAAGTGTGTGAACTTAAT 485
DB 523 CTCTTTGAGTTTGTGAGCTCTCAACTGCGGTTCACTGTGCTGAGGCTGTGAATTAAC 582
QY 486 AAGCAGCAGACGACATGCGCGGTGAATGGCTGGGCGCTGCACCATGCAAAAGATCC 545
DB 583 CGAACAACAGACTGATATGGCTGTAAATGGCTGAGGATTAATCAATGCTMAAATAATAC 642
QY 546 GAGGCATCTGCTCTGTGTAAGTATATCGTCTTGGCCATCCCTGGAACTGCTAAG 605
DB 643 GAAAGATCAGGATTTCTGTACGTTAATGATATATGCTGTCGATCCCTTGAATTAAG 702
QY 606 TATACACAGAGAGGCTGCTACTATGATGATTAATTCACATGCTGAGCGCGTGAAGAG 665
DB 703 TATCATGAGAGAGCTTATATATGATATATGATATTAATGATGATGATGATGATGAA 762
QY 666 GCTTTCTACACAGAGCGCGGTGATGATGCTGTCTTCTTAAGTATGAGAGTACTTC 725
DB 763 GCTTTTATATACAAAGATCGTGTATGACGCGTATCAATTCCTAAATATGGGGAATACCTT 822
QY 726 CCAGGAATGAGGAGCTTACGAGGATACGCGGCTGGCAAAAGCAATGTTATGCTGTTAAC 785
DB 823 CTGACACAGAGAGCTTGAAGGATTTGCTCTGAAAAGGCAAAATCTATGCTGTCAT 882
QY 786 TACCGCTCCGAGACGAGATTTGATGACGAGTCTTATGAGGCGCATTTTCAAGCCGATCAG 845
DB 883 TTTCCAAATGTGTGATGATATGATGATGATGATGATGATGATGATGATGATGATGATG 942
QY 846 TCCTAAAGTATGAGATGTTCCAGCTATGTCGGTGTCTTACAGTGTGCTCAAGTCC 905
DB 943 TCAAGGTGATGAGATGATGATCAACCTAGTGTGTGATTAACAGTGTGTGAGCACTCA 1002
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QY 906 CTATCTGGGAGTGGTATGAGTGTCTCAATCTATCTATCAAGAGACGCGAAGTGTG 965
DB 1003 TTATCTGATATATAGCTGGTGTGTTTAACTTAACAGTCAAAAGGTCAATGTTAATGTGTA 1062
QY 966 GAATTTGTCAAGACTTTAACTGCTATGCTGATGCTGAGAGCGGTGTTACCACTT 1025
DB 1063 GAAGTTTAAAACTTTAACTTAACATTAATGATGCTGATGCTGAGAGAGTGTACACATC 1122
QY 1026 CGTACGTTGCGCGGTCTGAGACATATGAGACAGCTGTGGCTCTGATAGAGAGATCTCCT 1085
DB 1123 CGTATGTTCTGATGTTGAGACATATGAGACATGCACTGCGCTGATTTGTGATGCC 1182
QY 1086 AATGAGCTTCATCAATGATGATCTATTTGATTTGATGATGATGATGATGATGATGATG 1145
DB 1183 AATGATGCTTCATTAATGATGATTTACTTTGATGATTTTGGACCAAGCTTCAATGATTT 1242
QY 1146 AGTCTTCCAAATATGATGATCAAGAACAGCAATGATGATGATGATGATGATGATGATG 1205
DB 1243 AGTCTTCAAAATGATGATCAAGAACAGCAATGATGATGATGATGATGATGATGATGATG 1302
QY 1206 CTGTTTGAAGACCTTGAATGCTGCGGACAGCACTTGGGTCCAAAGCGAGGATTCCT 1265
DB 1303 TTGTTGAAAATTTGGCATGTTAATCTCATGACCTGCTGTCCAGATGCAAGCTTATTTCA 1362
QY 1266 GAGGAGCGCATCCCTGAGAGAGTGGCGATGAGAGAGCAAGACGACCTGACAAAGCGCATC 1325
DB 1363 GAAGATGCTTTATGATGAGACAGTGAAGATGAGATGAGATGAGATGAGATGAGATGAGAT 1422
QY 1326 TCGATCTGCTCTCTGAACAAAGCAATGCTGCTGAGAGAGATTTCCGATTTGAAAG 1385
DB 1423 TCTATTTGACATCAAGCAAGCGGATGCTTGTGATGAAAGATTTCTCAGATTTGAGAT 1482
QY 1386 GAGGAGAGGAGGCGCGCAAGAACTTCTCACTTCAAAAAACCAAGAGATCAAAACA 1445
DB 1483 GAAAGAGAGAGAGTGAAGAAATGTGCTGATCATTAAGAAAGACAAAGAAAGCTTGA 1542
QY 1446 GAGATGAAAAGAGAAAGACCCAGAGAGAGAGAAAGAAATCAACCGAAGAGAGAAACC 1505
DB 1543 ATTGAAGAGATTAAGAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGATTA 1602
QY 1506 AAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1551
DB 1603 TCCAGAGACAAAGTGGTGAATAAAACGATACCAAGAGAACCAAT 1648

RESULT 14
AAC90323
ID AAC90323 standard; DNA; 1985 BP.
XX
AC AAC90323;
XX
DT 19-MAR-2001 (first entry)
XX
DE U1814 cDNA clone.
XX
XX
XX METH: metalloproteinase; thrombospondin; angiogenesis inhibition;
XX cancer therapy; benign tumour; ocular angiogenic disease;
XX rheumatoid arthritis; psoriasis; wound healing; endometriosis;
XX vasculogenesis; granuloma; hypertrophic scar; nonunion fracture;
XX scleroderma; trachoma; vascular adhesion; myocardial angiogenesis;
XX coronary collateral; cerebral collateral; arteriovenous malformation;
XX ischaemic limb angiogenesis; Osler-Weber syndrome; wound granulation;
XX plaque neovascularisation; telangiectasia; haemophilic joint; EST;
XX angiodioma; fibromuscular dysplasia; expressed sequence tag;
XX Crohn's disease; atherosclerosis; birth control; ss.
XX
XX Unidentified.
XX
XX MO200071577-A1.
XX
XX 30-NOV-2000.
XX
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Db 1603 TCAGAGACAACAGTGTGTAAGAAAAACAGATACCAAGAACCAAT 1648

RESULT 15

AAC89555

ID AAC89555 standard; DNA; 1985 BP.

XX AAC89555;

XX AAC89555;

XX 08-MAR-2001 (first entry)

XX

XX Human histone deacetylase HDAC-2 coding sequence.

XX

XX Histone deacetylase; HDAC-1; HDAC-2; HDAC-3; HDAC-4; HDAC-5; HDAC-C;

XX HDAC-D; cell cycle; tumorigenesis; cancer; inhibitor; antisense;

XX gene therapy; ds.

XX

XX Homo sapiens.

XX

XX MO200071703-A2.

XX

XX 30-NOV-2000.

XX

XX 03-MAY-2000; 2000WO-1B01252.

XX

XX 03-MAY-1999; 99US-0132287.

XX

XX (METH-) METHYLGENE INC.

XX

XX Macleod AR, Li Z, Beesterman JM;

XX

XX WPI: 2001-016407/02.

XX

XX P-PSDB; AAB49955.

XX

XX Antisense oligonucleotide that inhibits expression of a histone

XX deacetylase, useful for treating and/or alleviating the symptoms of

XX neoplasia, or for inhibiting neoplastic cell growth in an animal -

XX

XX PS Disclosure; Page 53; 125pp; English.

XX

XX The present invention provides inhibitors of histone deacetylase enzymes

XX such as HDAC-1, HDAC-2, HDAC-3, HDAC-4, HDAC-5, HDAC-C and HDAC-D. These

XX inhibitors may be antisense strands or they may be compounds identified

XX by contacting the enzyme with the compound and measuring the resulting

XX enzyme activity. These inhibitors are useful for treating cancers and for

XX identifying which histone deacetylase is involved in a neoplasia.

XX

XX Sequence 1985 BP; 626 A; 360 C; 454 G; 545 T; 0 other;

XX

XX Query Match 50.0%; Score 805.2; DB 22; Length 1985;

XX Best Local Similarity 72.8%; Pred. No. 3.5e-234; Indels 0; Gaps 0;

XX Matches 1038; Conservative 0; Mismatches 388;

Qy 126 GGCACCCCGAGAGAAAGTCTGTACTACTACGACGGGAGTGTGAAATTAATTAATGA 185

Db 223 GCGCGCAAAAAAAGTCTGTACTACTACGACGGTGTATTTGAAATTAATTAATGA 282

Qy 186 CAAGGCCCAACCAAGACCTTCACCGAATCCGATGATCTAATTTCTGCTCAACTAT 245

Db 283 CAGGGTCAATCCCAAGACCTTCATAGAAATCCGATGACCCATTAATTTCTGCTTAATTAAT 342

Qy 246 GGTCTCTACCAAAAAATGGAATCTATGCGCTCCCAAGAACCAATGAGAGATGACC 305

Db 343 GGGTATATCAGAAAAATGGAATATATAGCCCAATTAAGCCATGCGGAGAAATGCA 402

Qy 306 AAGTACCAAGAGATGATCAATTAATTTCTGCGCTCATCCGTCCAGATTAACATGTCG 365

Db 403 AAATATCAAGATGATGATATATCAATTTCTAGCGTCAATTAAGCCAGATTAACATGTC 462

Qy 366 GAGTACAGCAAGATGATGATCAATTTCTAGCGTCAATTTCTGATTTGATGATGATG 425

Db 463 GAGTATAGTAAAGATGATGATATATTTATGTTGAGAAATGATGATGATGATGATG 522

Qy 426 CTGTTGAGTCTGTCAATGCTACTGTGTGTTCTGTGCAAGTGTGAAACTTAAT 485

Db 523 CTCTTGAAGTTTGTGAGCTCTCACTGGCGGTTCAAGTTGTGAGCTGTGAAGTTAA 582

Qy 486 AAGCAGACAGCAATCGCCGTAATTTGGGCTGGGGCTGCAACCATGCAAAAGACTCC 545

Db 583 CGAACACAGACTGATGTGCTGTTAAATGGGCTGGAGATTACATCATGCTGAAGATAC 642

Qy 546 GAGGATCTGGCTTGTGATGATCAATGATATGCTGTGGCCATCTGCAACTGCTAAG 605

Db 643 GAGGATCAGGATTTCTGTTAGTAAATGATGTGCTGCTCCATCTGTAATTAATCAAG 702

Qy 606 TATCACCAGAGGATGCTGATCAATGATTAATTCACCATGATGATGATGATGATGATG 665

Db 703 TATCATCAGAGATCTTATATATGATTAATGATTAATCATGATGATGATGATGATG 762

Qy 666 GCTTTCTACACCAAGGATGATGATGATGATGATGATGATGATGATGATGATGATG 725

Db 763 GCTTTTATCAACAGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 822

Qy 726 CCAAGAACTGGGAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATG 785

Db 823 CTGACACAGAGATCTTGAAGGATTTGCTGCTGAAAGCAAAATCTATGCTGATAT 882

Qy 786 TACCCGCTCCGAGACGGGATGATGATGATGATGATGATGATGATGATGATGATGATG 845

Db 883 TTTCCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 942

Qy 846 TCCAAAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 905

Db 943 TCAAGGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1002

Qy 906 CTATCTGGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 965

Db 1003 TTATCTGATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1062

Qy 966 GAATTTGTCAAGACTTTAACTGCTATGATGATGATGATGATGATGATGATGATGATG 1025

Db 1063 GAAGTTGTAACCTTTAACTTAACTTAACTTAACTTAACTTAACTTAACTTAACTTAA 1122

Qy 1026 GATACCTTCCGAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATG 1085

Db 1123 GATACCTTCCGAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATG 1182

Qy 1086 AATGAGCTTCAATCAATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1145

Db 1183 AATGAGCTTCAATCAATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1242

Qy 1146 AGTCTTCCAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1205

Db 1243 AGTCTTCCAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1302

Qy 1206 CTGTTTGAAGACTTGAATGCTGCGGACGACCTTGGGTTCCAAAGCGATGATGATG 1265

Db 1303 TTGTTTGAAGACTTGAATGCTGCGGACGACCTTGGGTTCCAAAGCGATGATGATG 1362

Qy 1266 GAGGAGCAATCCCTGAGAGATGATGATGATGATGATGATGATGATGATGATGATGATG 1325

Db 1363 GAGGAGCAATCCCTGAGAGATGATGATGATGATGATGATGATGATGATGATGATGATG 1422

Qy 1326 TCGATCTGCTCTTGAAGCAATGCTGATGATGATGATGATGATGATGATGATGATGATG 1385

Db 1423 TCGATCTGCTCTTGAAGCAATGCTGATGATGATGATGATGATGATGATGATGATGATG 1482

Qy 1386 GAGGAGAGGGGCGGCAAGAACTTTCAATTTCAAAAGCGCAAGAGATCAAAACA 1445

Db 1483 GAGGAGAGGGGCGGCAAGAACTTTCAATTTCAAAAGCGCAAGAGATCAAAACA 1502

Qy 1446 GAGGAGAGGGGCGGCAAGAACTTTCAATTTCAAAAGCGCAAGAGATCAAAACA 1505

Db 1543 ATTGAAGATTAAGAAAGAAACGAGAGCAAAAGAAAGCGTTAAGAAAGATTAAG 1602

Qy 1506 AAGGAGAGAAAGCAAGAAAGCGGCTCAAGAGAGGCGCAAGT 1551

Db 1603 TCACAGACACAGTGTGTGAAAAACACAGATACCCAAAGAACCAAT 1648

Search completed: December 5, 2003, 14:07:54
Job time : 463 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: December 5, 2003, 13:51:42 / Search time 3170 Seconds
(without alignments)
12351.581 Million cell updates/sec

Title: US-09-817-913-2
Perfect score: 1611
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 22781392 seqs, 12152238056 residues

Total number of hits satisfying chosen parameters: 45562784

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
EST:*
1: em_estba:*
2: em_esthum:*
3: em_estin:*
4: em_estmu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_hic:*
9: gb_est1:*
10: gb_est2:*
11: gb_hic:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estcom:*
17: em_gse_hum:*
18: em_gse_inv:*
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20: em_gse_vrt:*
21: em_gse_fun:*
22: em_gse_mam:*
23: em_gse_mus:*
24: em_gse_pro:*
25: em_gse_rtd:*
26: em_gse_pbg:*
27: em_gse_vrl:*
28: gb_gse1:*
29: gb_gse2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match length | ID | Description |
|------------|--------|--------------------|---------|--------------------|
| 1 | 1152.6 | 71.5 | 1953 11 | AK076080 Mus muscu |
| 2 | 983.4 | 61.0 | 1201 13 | BX425368 BX425368 |
| 3 | 943.2 | 58.5 | 1201 9 | AL518877 AL518877 |
| 4 | 942.2 | 58.5 | 1201 13 | BX421673 BX421673 |

| | | | | | |
|----|-------|------|---------|----------|----------|
| 5 | 935.4 | 58.1 | 1201 9 | AL531607 | AL531607 |
| 6 | 903 | 56.1 | 1201 9 | AL546378 | AL546378 |
| 7 | 901.4 | 56.0 | 1201 13 | BX382026 | BX382026 |
| 8 | 900 | 55.9 | 970 9 | AL558916 | AL558916 |
| 9 | 886.2 | 55.0 | 932 13 | BQ925676 | BQ925676 |
| 10 | 885.6 | 55.0 | 1201 13 | BX333758 | BX333758 |
| 11 | 884.2 | 54.9 | 951 13 | BQ925328 | BQ925328 |
| 12 | 872.2 | 54.1 | 1062 13 | BQ276276 | BQ276276 |
| 13 | 863.8 | 53.6 | 897 13 | BQ642872 | BQ642872 |
| 14 | 860.2 | 53.4 | 1201 9 | AL541430 | AL541430 |
| 15 | 857.4 | 53.2 | 1201 9 | AL559849 | AL559849 |
| 16 | 843.2 | 52.3 | 961 14 | CD515346 | CD515346 |
| 17 | 841.6 | 52.2 | 1060 12 | BQ054741 | BQ054741 |
| 18 | 841.2 | 52.2 | 992 13 | BX458328 | BX458328 |
| 19 | 836.2 | 51.9 | 919 13 | BQ641927 | BQ641927 |
| 20 | 833.6 | 51.7 | 906 9 | AL546172 | AL546172 |
| 21 | 831 | 51.6 | 910 9 | AL522933 | AL522933 |
| 22 | 820.4 | 50.9 | 1015 13 | BQ064007 | BQ064007 |
| 23 | 805.2 | 50.0 | 1072 12 | BM923452 | BM923452 |
| 24 | 797.4 | 49.5 | 1627 11 | BC013141 | BC013141 |
| 25 | 789.2 | 49.0 | 954 10 | BG754715 | BG754715 |
| 26 | 780.4 | 48.4 | 858 13 | BH845191 | BH845191 |
| 27 | 779.4 | 48.4 | 910 10 | BG756668 | BG756668 |
| 28 | 778 | 48.3 | 982 12 | BM477303 | BM477303 |
| 29 | 775 | 48.1 | 919 13 | BQ423456 | BQ423456 |
| 30 | 773.8 | 48.0 | 864 13 | BQ521868 | BQ521868 |
| 31 | 769.2 | 47.7 | 918 13 | BQ679101 | BQ679101 |
| 32 | 768.4 | 47.7 | 854 13 | BH553962 | BH553962 |
| 33 | 760.8 | 47.2 | 929 12 | BQ057220 | BQ057220 |
| 34 | 760.8 | 47.2 | 967 13 | BQ680103 | BQ680103 |
| 35 | 754 | 46.8 | 852 12 | BQ218781 | BQ218781 |
| 36 | 748 | 46.4 | 1025 12 | BQ062801 | BQ062801 |
| 37 | 745.6 | 46.3 | 872 13 | BQ215409 | BQ215409 |
| 38 | 737.4 | 45.8 | 778 12 | BT727204 | BT727204 |
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ALIGNMENTS

RESULT 1
AK076080
LOCUS Mus musculus 11 days embryo whole body cDNA, RIKEN full-length
DEFINITION full insert sequence.
ACCESSION AK076080
VERSION AK076080.1 GI:26096626
KEYWORDS HTC; CAP trapper.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE
1 Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,
Itoh, M., Kono, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
JOURNAL
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2
Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,
Itoh, M., Kono, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new genes
Genome Res. 10 (10), 1617-1630 (2000)
JOURNAL
MEDLINE
PUBMED
11042159

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AUTHORS
3
Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Komno, H., Akiyama, J., Nishii, K., Kitsuana, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, R., Matsunoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujikawa, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watanabe, M., Ozonaki, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsura, S., Kawai, J., Ozaki, Y., Muramatsu, M., Inoue, Y., Kira, A., and Hayashizaki, Y.
RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer
Genome Res. 10 (11), 1757-1771 (2000)

TITLE
JOURNAL
MEDLINE
PUBMED
20530913
11076861

REFERENCE
AUTHORS
4
Kawai, J., Shinagawa, A., Shibata, K., Yoshino, M., Itoh, M., Ishii, Y., Aizawa, T., Hara, A., Fukunishi, Y., Komno, H., Adachi, J., Fukuda, S., Aizawa, K., Izawa, M., Nishi, K., Kiyosawa, H., Kondo, S., Yamana, I., Saito, T., Okazaki, Y., Gotohori, T., Bono, H., Kasukawa, T., Saito, R., Kadota, K., Matsuda, H., Ashburner, M., Batalov, S., Casavant, T., Fleischmann, W., Gaasterland, T., Gissi, C., King, B., Kochiwa, H., Kuehl, P., Lewis, S., Matsuo, Y., Nikaido, I., Pesole, G., Quackenbush, J., Schriml, L. M., Staudili, F., Suzuki, R., Tomita, M., Wagner, L., Washio, T., Sakai, K., Okido, T., Furuno, M., Aono, H., Baldarelli, R., Barsh, G., Blake, J., Boffelli, D., Bojunga, N., Carninci, P., de Bonaldo, M. F., Brownstein, M. J., Bull, C., Fletcher, C., Fujita, M., Gariboldi, M., Gustincich, S., Hill, D., Hotmann, M., Hume, D. A., Kamita, M., Lee, N. H., Lyons, P., Mochizumi, L., Mashima, J., Mazzaletti, J., Mombauts, P., Nordone, P., Ring, B., Ringwald, M., Rodriguez, I., Sakamoto, N., Sasaki, H., Saito, K., Schenbach, C., Seya, T., Shibata, K. P., Storch, K. P., Suzuki, H., Toyooka, K., Wang, K. H., Weitz, C., Whitaker, C., Wilmberg, L., Wyshew-Boris, A., Yoshida, K., Hasegawa, Y., Kawaji, H., Kohsaki, S., and Hayashizaki, Y.
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Nature 409 (6821), 685-690 (2001)

TITLE
JOURNAL
MEDLINE
PUBMED
21085660
11217851

REFERENCE
AUTHORS
5
The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.
Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
Nature 420, 563-573 (2002)

TITLE
JOURNAL
REFERENCE
AUTHORS
6 (bases 1 to 1953)

ADACHI, J., AIZAWA, K., AKAHIRA, S., AKIMURA, T., AONO, H., ARAI, A., ARAKAWA, T., BONO, H., CARNINCI, P., FUKUDA, S., FUKUNISHI, Y., FURUNO, M., HANAGAKI, T., HARA, A., HAYASE, N., HIRAMOTO, K., HIRAO, T., HORI, F., IMOTANI, K., ISHII, Y., ITOH, M., IZAWA, M., KASUKAWA, T., KATO, H., KAWAI, J., KOJIMA, Y., KOMNO, H., KOWA, M., KOYA, S., KURIHARA, C., MATSUYAMA, T., MIYAZAKI, A., NISHII, K., NOMURA, K., NUMAZAKI, R., OHNO, M., OKAZAKI, Y., OKIDO, T., OWA, C., SAITO, H., SAITO, R., SAKAI, C., SAKAI, K., SANO, H., SASEKI, D., SHIBATA, K., SHIBATA, Y., SHINAGAWA, A., SHIRAKI, T., SOGABE, Y., SUZUKI, H., TAGAMI, M., TAGAWA, A., TAKAHASHI, F., TANAKA, T., TEJIMA, Y., TOYA, T., YAMAMURA, T., YAMANAKA, I., YASUNISHI, A., YOSHIDA, K., YOSHINO, M., MURAMATSU, M., and HAYASHIZAKI, Y.
Direct Submission
Submitted (16-APR-2002) Yoshihide Hayashizaki. The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute, 1-7-22 Suehiro-cho, Tsukuba-shi, Yokohama, Kanagawa 230-0045, Japan (E-mail: genome-res@gsc.riken.go.jp, URL: http://genome.gsc.riken.go.jp/, Tel: 81-45-503-9222, Fax: 81-45-503-9216)

COMMENT
cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.
Please visit our web site for further details.
URL: http://genome.gsc.riken.go.jp/
URL: http://fantom.gsc.riken.go.jp/
Location/Qualifiers

FEATURES

source
1. 1953
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6J"
/db_xref="FANTOM_DB:2700094A20"
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Matches 1301; Conservative 0; Mismatches 174; Indels 4; Gaps 4;

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78 CAAGGACCCCAATGAAAGCTCAACCGAATCCGATGACTATTAATTGCTCACTAT 137
246 GGTCTTACCGAAATGAAATCTATCGCCCTCACAAAGCCAAATGCTGAGAGATACC 305
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306 AAGTACCAAGCATGATCTATTAATTCTTGGCTCCATCCGTCAGATTAATCTG 365
198 AAGTACCAAGCATGATCTATTAATTCTTGGCTCCATCCGTCAGATTAATCTG 257
366 GAGTACCAAGCATGATCTATTAATTCTTGGCTCCATCCGTCAGATTAATCTG 425
258 GAATACCAAGCATGATCTATTAATTCTTGGCTCCATCCGTCAGATTAATCTG 317
426 CTGTTGAGTCTGCTGATGTTGCTACTGTTGCTGCTGCTGCTGCTGCTGCTGCT 485
318 TTGTTGAGTCTGCTGATGTTGCTACTGTTGCTGCTGCTGCTGCTGCTGCTGCT 377
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498 TATCACCAGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 557
666 GCTTCTACACCAAGCATGATCTATTAATTCTTGGCTCCATCCGTCAGATTAATCTG 725
558 GCTTCTACACCAAGCATGATCTATTAATTCTTGGCTCCATCCGTCAGATTAATCTG 617
726 CCGAAGCTGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 785
618 CCGAAGCTGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 677
786 TACCCGCTCCAGAGCGGATTTGATGACGATCTTATGAGCCATTTTCAAGCCGCTCATG 845
678 TACCCGCTCCAGAGCGGATTTGATGACGATCTTATGAGCCATTTTCAAGCCGCTCATG 737
846 TCCAAAGTATGAGATGTTCCAGCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCT 905
738 TCCAAAGTATGAGATGTTCCAGCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCT 797

| | | | | |
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| QY | | 906 | CTATCTGGGAGTCCGTTAGTTGTCTCAATCTATCTATCAAGAAGACAGCCAAGTGTCG | 965 |
| Db | | 798 | CTGTCTGGGAGCCGGTTAGTTGTCTTCAATCTGAGCATC- AAGACACGCCAAGTGTCG | 856 |
| QY | | 966 | GAATTGTGCAGAGCTTTAACTTCGCTCATGTGTAGTCTGGAGGCGGTGTACTAACCAT | 1025 |
| Db | | 857 | GAGTTCGTAAGAGTTTCAACTTGCCCATGTGATGTCTGGAGGAGGTGTACTAACCATC | 916 |
| QY | | 1026 | CCTAACCTTGGCCCCGGTGTCTGACATATGACAAGCTGTGGCCCCCTGAGATACGGAGTCCCT | 1085 |
| Db | | 917 | CGGAATGGTGTCTGCTGTCTGACATTAACMAACAGCGGTGTGGCCCTTTGACACAGAGATCCCT | 976 |
| QY | | 1086 | AATAGAGCTTCATATCAATGACTACTTTGAATACTTTGACACAGATTTCAACTCCACATC | 1145 |
| Db | | 977 | TATAG- TGGCCCTACACGACTTACTTTGAATACTTTGACACGAGATATATCTCTTACATC | 1035 |
| QY | | 1146 | AGTCCTTCCAAATATGACTTAACCCAGAACACGATGAGTACTCTGAGAAATCAACACAGCA | 1205 |
| Db | | 1036 | AGGCCCTTCCAAATATGACCAACCAAGAACACTAACCAGATACCTGAGAAATATCAGGAGCGT | 1099 |
| QY | | 1206 | CTGTTTGAAGAACCTTAGATCTCTGCGACGCACTTGSGGTCCAAACGACAGCGCATTCCT | 1265 |
| Db | | 1096 | CTCTTTGAGAACTTGAGGATGCTGCGCCATGCCCT- GGGTTCAGATGACAGCCATCCCT | 1155 |
| QY | | 1266 | GAGGACGCCATCCCTGAGAGAGATGAGCGCATGAGACGAAACGACCCCTGACAAAGCGCATC | 1325 |
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| QY | | 1326 | TCCATCTGCTCCTCTGACAAACGAAATTCCTGTGAGAAAGATTCTCCGATTTCTGAAAG | 1385 |
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| Db | | 1395 | AAGAGAGAGAACCCAGAGCCAAAGGGGTCAAGAAAGAGTCAAGTTGGCTTG- AGCAAG | 1455 |
| QY | | 1566 | CTCTCAAGCTCTGCTTCCTGCTGAGTCCCTCACGTTTTC | 1604 |
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| LOCUS | BX425368 | 1201 bp | mRNA | linear EST 15-MAY-2003 |
| DEFINITION | BK425368 Homo sapiens NEUROBLASTOMA Homo sapiens CDNA clone | | | |
| VERSION | CL0BB011ZHI1.5-PRIME, mRNA sequence. | | | |
| ACCESSION | BK425368 | | | |
| KEYWORDS | BK425368.1 GI:30770463 | | | |
| SOURCE | EST. | | | |
| ORGANISM | Homo sapiens (human) | | | |
| REFERENCE | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; | | | |
| AUTHORS | Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. | | | |
| JOURNAL | L.I.W.B., Gruber,C., Jeessee,J. and Polayes,D. | | | |
| COMMENT | Full-length cDNA libraries and normalization | | | |
| | Unpublished | | | |
| | Contact: Genoscope | | | |
| | Genoscope - Centre National de Sequencage | | | |
| | BP 191 91006 Evry cedex - France | | | |
| | Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr | | | |
| | Library was constructed by Life Technologies, a division of | | | |
| | Invitrogen. This sequence belongs to sequence cluster 884.f For | | | |
| | more information about this cluster, see | | | |
| | http://www.genoscope.cns.fr/ | | | |

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cgi-bin/cluster.cgi?seq=Cl0BB011ZH1RP1&cluster=884.f. Contact
Feng Liang Email : fliang@life.techn.com URL :
http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
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Location/Qualifiers
1..1201 ..
source

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/notes="Vector: pcwmsport 6; 1st strand cDNA was primed
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double-strand cDNA was digested with Not I and cloned into
the Not I and EcoRV sites of the pcwmsport 6 vector.
Library was not normalized."

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| Matches 1018; | Conservative 11; | Mismatches 13; | Indels 3; | Gaps 3; |
| QY | 97 | GGAGGCGAGCAAGTGGCGGCAAGCGAGGCGACCCGGAGGAAAGTCTGTTACTACTACG | 156 | |
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| Db | 150 | AACGGGATGTTGGAAAATHACTATTATGGACAAGGCCACCAATGAAAGCTCACCGAATCC | 209 | |
| QY | 217 | GCATGACTCATTAATTTGGCTCTCAACTATGATGTCCTACCGAAAATGAAATCTATCGCC | 276 | |
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| QY | 277 | CTCACAAAAGCCAAATGCTGAGAGATGCAAGTACCAAGGATGACTCATTTAAATTCCT | 336 | |
| Db | 270 | CTCACAAAARCCAAATGCGAGAGATGACCAAGTACCAAGGATGACTCATTTAAATTCCT | 329 | |
| QY | 337 | TGGGCTCCACATCCGTCGCGCATTAACATGTCGGAGTACAGCAAGCCAGATCCAGAGATTCAACG | 396 | |
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| QY | 397 | TTGGTGGAGACTGTCAGTATTCGATGGCCCTGTTGAGTTCTTGTCAGTTGTCATCTGGTG | 456 | |
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| QY | 457 | GTTCTGTGGCAAGTGTCTGTGAAACTTAATAAGCAGCAGACGGACATCGCGGTGAATGGG | 516 | |
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| Db | 510 | CTGGGGGCTTGGCACCATGCAAAARAAAGTCGAGGATCTGGCTTCTGTTACGTCATATGTA | 569 | |
| QY | 577 | TGCGCTTGGGCGCATCTTGGAACTGCTAAAGTATCACAGAGGTCCTGTACATTGACATTG | 636 | |
| Db | 570 | TGCGCTTGGGCGCATCTTGGAACTGCTAAAGTATCACAGAGGTCCTGTACATTGACATTG | 629 | |
| QY | 637 | ATATTTCCAAATGTTGACGCGCGTGGAAAGGCTTTCTAACACCAAGACCGGATCATGACTG | 696 | |
| Db | 630 | ATATTTCCAAATGTTGACGCGCGTGGAAAGGCTTTCTAACACCAAGACCGGATCATGACTG | 689 | |
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| | | | |
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| Db | 810 | CCTATGAGGCCATTTTCAGCCGGTCATGTCCAAAGTAATGAGATGTTCCAGCCTA | 869 |
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| Db | 1049 | CAGCTGTGGCCCTGGATACGGAGATCCCTTAATGAGCTT - CATACATGACT - MYTTKAAT | 1106 |
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| RESULT 3 | AL518877 | 1201 bp | mRNA | linear | EST 12-MAY-2003 |
|------------|---|---------|------|--------|-----------------|
| LOCUS | AL518877 | | | | |
| DEFINITION | AL518877 Homo sapiens NEUROBLASTOMA Homo sapiens CDNA clone | | | | |
| | CSDDA011YC11 5-PRIME, mRNA sequence. | | | | |

| | | |
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| ACCESSION | AL518877 | GI:30537616 |
| VERSION | AL518877.2 | |
| KEYWORDS | EST | |
| SOURCE | Homo sapiens (human) | |
| ORGANISM | Homo sapiens | |

REFERENCE
1 (bases 1 to 1201)
AUTHORS
Li, M.B., Gruber, C., Jesssee, J. and Polayes, D.
TITLE
Full-length cDNA libraries and normalization
JOURNAL
Unpublished
COMMENT
On Feb 13, 2001 this sequence version replaced gi:12782370.

Contact: Genoscope
Genoscope - Centre National de séquençage
BP 191 91006 EVRY cedex - France
Email: segret@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 884.f For
more information about this cluster, see
[http://www.genoscope.cns.fr/
cgl-bin/cluster.cgi?seq=CSD0A011AD06OP1&cluster=884.f](http://www.genoscope.cns.fr/cgl-bin/cluster.cgi?seq=CSD0A011AD06OP1&cluster=884.f). Contact :
Feng Liang Email : liang@lifetech.com URL :
<http://fulllength.invitrogen.com/InvitrogenCorporation1600>
Paradey Avenue Genoscope sequence ID : CSD0A011AD06OP1.

| FEATURES | Location/Qualifiers |
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/notes="Vector: pCMVSPORT 6; 1st strand cDNA was primed
with a NotI-oligo(dT) primer. Five prime end enriched,
the NotI and EcoRV sites of the pCMVSPORT 6 vector.
Library was not normalized."
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ORIGIN

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| QY | 397 | TTGGTGAAGACTGTCCAGTATTCGATGAGCGCTGTGAGTTCTGTCAATTGCTACTGCTG | 456 |
| Db | 374 | TTGGTGAAGACTGTCCAGTATTCGATGAGCGCTGTGAGTTCTGTCAATTGCTACTGCTG | 433 |
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| QY | 577 | TGCTCTGGGCGCATCTGGAACTGCTTAAGATACACAGAGGTCCTGTACATTGACATTG | 636 |
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| Db | 733 | CTGGCAAAAGCAATATTATGCTGTTAACTACCGGCTCCGAGACGGGATTTATGACGAGT | 792 |
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| QY | 877 | CGGTCGCTTTCACAGTGGGCTCAACATCCCATCT - GGGGATTCGGTTAAGTGTGCTTCAAT | 935 |
| Db | 853 | CGGTCGCTTTCACAGTGGGCTCAACATCCCATCT - GGGGATTCGGTTAAGTGTGCTTCAAT | 912 |
| QY | 936 | CTATCTATCAAGAGACACGCCAAGTGTGTGAATTTGTCAAGACTTTAACTTCACTGATG | 995 |
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| Db | 973 | CYGATGCTGGAGGGGGTGTAAACCATTCGTAACTTGCCCGGTGCTGACAAATGAG | 1032 |
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| RESULT 4 | | | | |
| BX421673 | | | | |
| LOCUS | BX421673 | 1201 bp | mRNA | linear |
| DEFINITION | BX421673 Homo sapiens T CELLS (JURKAT CELL LINE) Homo sapiens cDNA | | | EST 15-MAY-2003 |

| Accession | Version | Keywords | Source | Organism | Reference | Authors | Title | Journal | Comment |
|--|-------------|---------------|--------|----------|-----------|---------|-------|---------|---------|
| clone CSODH003YE10 | 5-PRIME | mRNA sequence | | | | | | | |
| BX421673 | | | | | | | | | |
| BX421673.1 | GI:30764107 | | | | | | | | |
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| Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; | | | | | | | | | |
| Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo. | | | | | | | | | |
| 1 (bases 1 to 1201) | | | | | | | | | |
| Full-length cDNA libraries and normalization | | | | | | | | | |
| Unpublished | | | | | | | | | |
| Contact: Genoscope | | | | | | | | | |
| Genoscope - Centre National de Sequencage | | | | | | | | | |
| BP 191 91006 Evry cedex - France | | | | | | | | | |
| Email: segefe@genoscope.cns.fr, Web : www.genoscope.cns.fr | | | | | | | | | |
| Library was constructed by Life Technologies, a division of | | | | | | | | | |
| Invitrogen. This sequence belongs to sequence cluster 884.f For | | | | | | | | | |
| more information about this cluster, see | | | | | | | | | |
| http://www.genoscope.cns.fr/ | | | | | | | | | |
| cgi-bin/cluster.cgi?seq=CSODH003C05QPL&cluster=884.f. Contact : | | | | | | | | | |
| Feng Liang Email : fliang@life.techn.com URL : http://fulllength.invitrogen.com/ | | | | | | | | | |
| http://fulllength.invitrogen.com/Invitrogen Corporation 1600 | | | | | | | | | |
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| /note="Vector: pCMVSPORT 6; 1st strand cDNA was primed | | | | | | | | | |
| with a NotI-Oligo(dT) primer. Five prime end enriched, | | | | | | | | | |
| double-strand cDNA was digested with Not I and cloned into | | | | | | | | | |
| the Not I and EcoRV sites of the pCMVSPORT 6 vector. | | | | | | | | | |
| Library was not normalized." | | | | | | | | | |
| BASE COUNT | | | | | | | | | |
| 304 a 260 c 300 g 282 t 55 others | | | | | | | | | |
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| Oy | | 1115 | ATACCTTGGACCAAGATTTCGAAGTCCACATCAAGTCCCTCCATATGATCTAACAGGAAC | 1174 |
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| Oy | | 1175 | : | |
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| LOCUS | | AL531607 Homo sapiens FETAL LIVER Homo sapiens cDNA clone | | |
| DEFINITION | | CS0DM002.HIS 5-PRIME, mRNA sequence. | | |
| ACCESSION | | AL531607 | | |
| VERSION | | AL531607.2 | | |
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| AUTHORS | | Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo. | | |
| TITLE | | 1. (bases 1 to 1201) | | |
| JOURNAL | | L.I.W.B., Gruber,C., Jessee,D. and Polayes,D. | | |
| COMMENT | | Full-length cDNA libraries and normalization | | |
| | | Unpublished | | |
| | | On Feb 13, 2001 this sequence version replaced gi:12795100. | | |
| | | Contact: Genoscope | | |
| | | Genoscope - Centre National de Sequencage | | |
| | | BP 191 91006 EVRY cedex - France | | |
| | | Email: seqref@genoscope.cns.fr Web : www.genoscope.cns.fr | | |
| | | Library was constructed by Life Technologies, a division of | | |
| | | Invitrogen. This sequence belongs to sequence cluster 884.f. For | | |
| | | more information about this cluster, see | | |


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QY 487 AGCAGACGACGACATCGCGTGAATTGGGCTGGGGCTTGACCAATGCAAGAAAGTCCG 546
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RESULT 7
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DEFINITION
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VERSION
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AUTHORS
TITLE
JOURNAL
COMMENT
Unpublished
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by life technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 884.f For
more information about this cluster, see
http://www.genoscope.cns.fr/
cgl-bin/cluster.cgi?seq=CSODI073CF040P1e:cluster=884.f. Contact :
Peng Liang Email : eliang@life.com URL :
http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
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Db 487 AAAAATATCCGAGGACATCTGCTCTGTAGTCAAGATATCTCTTTGGCCATCTTGA 546
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VERSION AL558916.2 GI:31283049
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ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 970)
Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
Full-length cDNA libraries and normalization
Unpublished
On Feb 15, 2001 this sequence version replaced gi:12903904.
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 Evry cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen. This sequence belongs to sequence cluster
884.f For more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CS0DJ007DH100P1cluster=884.f. Contact :
Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
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sites of the pCMVSPORT 6 vector. Library was normalized."
BASE COUNT 251 a 218 c 257 g 233 t 11 others
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Query Match 55.9%; Score 900; Db 9; Length 970;
Best Local Similarity 98.6%; Pred. No. 6.5e-147;
Matches 897; Conservative 9; Mismatches 4; Indels 0; Gaps 0;

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Db 61 GGGAGCGCAAGATGCGCGCAGACCGAGGACCCGGAGGAAAGTGTACTACTACG 120
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Db 601 ATATTCCATGATGAGACGCGGTGGAAGAGCCCTTTTACACACGAGCCGGGTATGACTG 660
Qy 697 TGTCTTTTCAATGATGAGAGTACTCTCCAGAGAACTGGGAACTTACCGGATACCGGG 756
Db 661 TGTCTTTTCAATGATGAGAGTACTCTCCAGAGAACTGGGAACTTACCGGATACCGGG 720
Qy 757 CTGGCAAGCAAGTATTATGCTTTAATACCGGCTCGAGACGGGATGATGACGAGT 816
Db 721 CTGGCAAGCAAGTATTATGCTTTAATACCGGCTCGAGACGGGATGATGACGAGT 780
Qy 817 CCTATGAGGCAATTTTCAAGCCGCTCATGTCGCAAGATGAGATGTTCCAGCTTATG 876
Db 781 CCTATGAGGCAATTTTCAAGCCGCTCATGTCGCAAGATGAGATGTTCCAGCTTATG 840
Qy 877 CGGTGCTTACAGTGTGCTCAGACTCCCTATCTGGGATCGGTTAGTGTGCTTCAATC 936
Db 841 CGGTGCTTACAGTGTGCTCAGACTCCCTATCTGGGATCGGTTAGTGTGCTTCAATC 900

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QY 937 TATCTATCAAGACACGCCAAGTGTGTGAATTTGTCAAGAGCTTTAACTTCCTATGC 996
 DB 901 TAACTATCAABAGACACGCCAAGTGTGTGAATTTGTCAAGAGCTTTAACTTCCTATGC 960
 QY 997 TGAATGCTGGG 1006
 DB 961 TGAATGCTGGG 970

RESULT 9
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 LOCUS AGENCOURT_8804320 NIH_MGC_47 Homo sapiens cDNA clone IMAGE:6377915
 DEFINITION 5', mRNA sequence.
 ACCESSION B0926976
 VERSION B0926976.1 GI:22342007
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Reference: Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 NIH-MGC http://mgi.nci.nih.gov/
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished
 Contact: Robert Strausberg, Ph.D.
 Email: cgaabs-remail.nih.gov
 Tissue Procurement: ATCC
 CDNA Library Preparation: Rubin Laboratory
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at: http://image.lnl.gov
 Plate: LHC8562 row: h column: 12
 High quality sequence stop: 668.
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 /tissue_type="neuroblastoma, cell line"
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 /clone_lib="NIH_MGC_47"
 /note="Organ: Brain; Vector: pOTB7; Site:1: XhoI; Site:2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCAAGAG(G). Size selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC Library."

BASE COUNT 235 a 209 c 248 g 240 t
 ORIGIN

Query Match 55.0%; Score 886.2; DB 13; Length 932;
 Best Local Similarity 97.0%; Pred. No. 1.6e-144;
 Matches 903; Conservative 0; Mismatches 28; Indels 0; Gaps 0;

QY 286 CCAATGCTGAGAGACCAAGATGACAGAGGATGACTTAAATCTTGCGCTCCA 345
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 DB 62 TCCGTCAGATTAATGTCGAGATGACAGAGGATGACAGATTCAGCTTGAGG 121
 QY 406 ACTGTCAGATTCAGATGCTGTTGAGTTCGTCACTGTTCTACTGCTGCTTCTG 465
 DB 122 ACTGTCAGATTCAGATGCTGTTGAGTTCGTCACTGTTCTACTGCTGCTTCTG 181

QY 466 CAAATGCTGTGAATCTTAATAGCAGACGACATCCCGTGAATTTGGCTGGGGCC 525
 DB 182 CAAATGCTGTGAATCTTAATAGCAGACGACATCCCGTGAATTTGGCTGGGGCC 241
 QY 526 TGAACATGCAAGAAAGTCCGAGGCACTTGGCTTCTGTTACGTCAATGATATGCTTGG 585
 DB 242 TGAACATGCAAGAAAGTCCGAGGCACTTGGCTTCTGTTACGTCAATGATATGCTTGG 301
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 QY 646 ATGCTGACGCGGTGGAAGAGGCTTCTACACACAGAGCGGTCACTGATGCTCTTTC 705
 DB 362 ATGCTGACGCGGTGGAAGAGGCTTCTACACACAGAGCGGTCACTGATGCTCTTTC 421
 QY 706 ATTAATATGAGAGATCTTCCAGAGACTGGGGACTTACGGGATACCGGGGCTGGCAAG 765
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 QY 766 ACAAGTATTAATGCTGTTAATACCGGCTCGAGAGCGGATGATGAGAGTCTATGAG 825
 DB 482 GCAAGTATTAATGCTGTTAATACCGGCTCGAGAGCGGATGATGAGAGTCTATGAG 541
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 DB 602 TACAGTGTGCTCAGACTCCCTATCTGGGATGCGGTAGGTGCTTCAATCTATATCA 661
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 QY 1006 GAGCGCGGTGTTACACATCTGTAAGCTTCCCGGTGCTGAGACATATGAGACGCTGG 1065
 DB 722 GAGCGCGGTGTTACACATCTGTAAGCTTCCCGGTGCTGAGACATATGAGACGCTGG 781
 QY 1066 CCCTGATACGAGATGCTCTTAATGAGCTTCCATACATGATCTTGAATCTTTGAC 1125
 DB 782 CCCTGATACGAGATGCTCTTAATGAGCTTCCATACATGATCTTGAATCTTTGAC 841
 QY 1126 CAGATTTCAAGCTCCACATCACTGCTTCCAAATGATCTAACCAAGACAGATGATACC 1185
 DB 842 CAGATTTCAAGCTCCACATCACTGCTTCCAAATGATCTAACCAAGACAGATGATACC 901
 QY 1186 TGGAGAAGATCAACAGAGGACTGTTGAGAA 1216
 DB 902 CTGGAGAAGATCAACAGAGGACTGTTGAGAA 932

RESULT 10
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 LOCUS BX333758
 DEFINITION CDNA clone CS0DD001Y16 5-PRIME, mRNA sequence.
 ACCESSION BX333758
 VERSION BX333758.1 GI:30333251
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Reference: Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 Li, W.B., Gruber, C., Jesse, J. and Polayes, D.
 Full-length cDNA libraries and normalization
 Unpublished
 Contact: Genoscope
 Genoscope - Centre National de Sequencage
 BP 191 91006 EVRY cedex - France
 Email: segr@genoscope.cns.fr, Web : www.genoscope.cns.fr

Library was constructed by Life Technologies, a division of Invitrogen. This sequence belongs to sequence cluster 884.f. For more information about this cluster, see <http://www.genoscope.cns.fr/cgi-bin/cluster.cgi?seq=CS0DD001B808Q1&cluster=884.f>. Contact : Feng Liang Email : liang@lifetech.com URL : <http://fulllength.invitrogen.com/> Invitrogen Corporation 1600 Faraday Avenue Genoscope sequence ID : CS0DD001B808Q1.

FEATURES

SOURCE

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/clone_lib="Homo sapiens NEUROBLASTOMA COT 50-NORMALIZED"
/note="1st strand cDNA was primed with a NotI-oligo (dt) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized."

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BASE COUNT 308 a 262 c 320 g 280 t 31 others

ORIGIN

Query Match 55.0%; Score 885.6; DB 13; Length 1201;
 Best Local Similarity 97.0%; Pred. No. 2e-144;
 Matches 939; Conservative 5; Mismatches 19; Indels 5; Gaps 4;

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Qy 97 GGGAGGCGAGCAAGATGGCGGAGACGCGAGGACCCCGAGAAAGTCTGTACTACTACG 156
Db 118 GGGAGGCGAGCAAGATGGCGGAGACGCGAGGACCCCGAGAAAGTCTGTACTACTACG 177
Qy 157 ACGGGAGTGTGAAGTACTATTATGGAAGAAGCCACCATGAAGGCTCCACCGAATCC 216
Db 178 ACGGGAGTGTGAAGTACTATTATGGAAGAAGCCACCATGAAGGCTCCACCGAATCC 237
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Db 238 GCATGACTCATTAATTTGCTGCTCAACTATGCTCTTACCGAAATGGAATCTATGCCC 297
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Db 298 CTCACAAAGCCAAAGTCTGAGAGATGACCAAGTACCAAGGATGACTACTTAATTTCT 357
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Db 418 TTGGTGAAGACTGTCAGATTTGATGAGCTGTTGATGCTGTCACTTGTCTACGCTG 477
Qy 457 GTTCTGAGCAAGTCTGTAACCTTAATAGACAGACAGGATCGCCCTGAATGGG 516
Db 478 GTTCTGAGCAAGTCTGTAACCTTAATAGACAGACAGGATCGCCCTGAATGGG 537
Qy 517 CTGGGGGGCTCAGCAGATGCAAGAAGTCCGAGGATCTGGCTTCTGTAACTCAATGATA 576
Db 538 CTGGGGGGCTCAGCAGATGCAAGAAGTCCGAGGATCTGGCTTCTGTAACTCAATGATA 597
Qy 577 TCGCTTTGGCCATCTGGAACTGCTAAAGTATCAACAGAGGCTGCTGATGACATTTG 636
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Qy 637 ATATTACACATGATGAGCGGCTGGAAGAGGCTTCTACACACAGGACCGGGTCACTG 696
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Qy 697 TGTCTTTTCAATGATGAGAGTACTTCCAGGAAGCTGGGAGCTCAAGGATACCGGGG 756
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Db 777 CTGGCAAGACAGATTAATGCTGTAACTACCGGCTCCAGACGGGATGATGACAGT 836
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Db 837 CCTATGAGGCATTTTCAAGCCGGTCAATGTCCAAAGTATGAGATGTCACGCTAGTG 896
Qy 877 CGGTGTCTTACAGTGTGCTCAAGTCCCTATCTGGG-GATCGGTTAGGTTCTTCAT 935
Db 897 CGGTGTCTTACAGTGTGCTCAAGTCCCTATCTGGGCGATCGGTTAGGTTCTTCAT 956
Qy 936 CTATCTTACAAAGACACCGCAAGTGTGTGGAATTTGTCAAGGC-TTTAACTGCTAT 994
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Qy 995 GCGATGCTGGAGGCGGTGTGTTACACATTGCTGAAGTCCCGGTCGTCGACATATGA 1054
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Db 1075 MACCGTTG 1082

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RESULT 11
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 DEFINITION 5', mRNA sequence.
 ACCESSION BQ925328
 VERSION BQ925328.1 GI:22340359
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 951)
 AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>;
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgabs-r@mail.nih.gov
 Tissue Procurement: DCTD/DTF/Gardar
 cDNA Library Preparation: Rubin Laboratory
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LINL at:
<http://image.llnl.gov>
 Plate: LLCM2605 row: h column: 07
 High quality sequence stop: 665.
 Location/Qualifiers

FEATURES

SOURCE

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/db_xref="taxon:9606"
/clone="IMAGE:6424758"
/issue_type="large cell carcinoma"
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/clone_lib="NIH_MGC_18"
/note="Organ: lung; Vector: pOTB7; Site 1: XhoI; Site 2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCAGAG(G). Library constructed by Ling Hong in the Laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC Library."

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BASE COUNT 236 a 216 c 253 g 238 t 8 others

ORIGIN

Query Match 54.9%; Score 884.2; DB 13; Length 951;
 Best Local Similarity 96.5%; Pred. No. 3.7e-144;
 Matches 920; Conservative 0; Mismatches 31; Indels 2; Gaps 2;

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DB 61 ACATGTCGAGTACAGACAGACAGATGACAGATTCACGTTGGTAGAGTCTCCAGTAT 120
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DB 121 TCATGAGGCTGTTGAGTCTGTCAGTCTGTCAGTCTGTCAGTCTGTCAGTCTGTCAG 180
QY 478 AACCTAATAAGACAGACAGACAGATGACAGATTCACGTTGGTAGAGTCTCCAGTAT 537
DB 181 AACCTAATAAGACAGACAGACAGATGACAGATTCACGTTGGTAGAGTCTCCAGTAT 240
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QY 658 TGAAGAGGCTCTTACACACAGGACCGGAGTACGTCGTCCTTCAATGATGAG 717
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QY 718 AGTACTCCGAGGACCTGAGGACCTGAGGATACCGGAGCTGAGGACCTGAGGATAT 777
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QY 958 AGTGTGGAATTTGTCAAGAGCTTTAAGTCTGCTATGCTGATGCTGAGGCGGTGTT 1017
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QY 1018 ACACCAATGTTAGTGGGCTGAGCATATGACAGGCTGAGGCTGAGGATACG 1077
DB 721 ACACCAATGTTAGTGGGCTGAGCATATGACAGGCTGAGGCTGAGGATACG 780
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RESULT 12
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DEFINITION AGENCOURT_6822351 NIH_MGC_111 Homo sapiens cDNA clone IMAGE:5931965
5', mRNA sequence.
ACCESSION B0276276
VERSION B0276276.1 GI:20486484

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KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 1062)
AUTHORS NIH-MGC http://mhc.nci.nih.gov/
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cga@bbs-r@mail.nih.gov
Tissue Procurement: CGAP (Stanford)
CDNA Library Preparation: Rubin Laboratory
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LHC2114 row: c column: 06
High quality sequence stop: 682.
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/tissue_type="cardioma, cell line"
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/clone_lib="NIH_MGC_111"
/note="Organ: prostate; Vector: pOTB7; Site 1: EcoRI;
Site 2: XhoI; cDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the
following 5' adaptor: TGGCAGAG(G). Library constructed by
Ling Hong in the laboratory of Gerald M. Rubin (University
of California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC Library."
BASE COUNT 276 a 248 c 284 g 254 t
ORIGIN
Query Match 54.1%; Score 87.2; DB 13; Length 1062;
Best Local Similarity 95.9%; Pred. No. 4.4e-142;
Matches 939; Conservative 0; Mismatches 33; Indels 7; Gaps 4;
QY 97 GGGAGGCGAGCAAGATGGGCGACAGCCAGCCAGGAGAAAGTCTGTTACTTACG 156
DB 13 GGGAGGCGAGCAAGATGGGCGACAGCCAGCCAGGAGAAAGTCTGTTACTTACG 72
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QY 277 CTCACAAAGCAATGTGAGAGATGACCAAGTACCAAGCCATGACTATTAATTTCT 336
DB 193 CTCACAAAGCAATGTGAGAGATGACCAAGTACCAAGCCATGACTATTAATTTCT 252
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DB 313 TTGTTGAGGACTGTCCAGTATTCGATGAGGCTGTTGAGTCTGTCAGTCTGTCAGTCTG 372
QY 457 GTTCTGTGCAAGTGTGTGAAACTTAATTAAGCAGACAGGACATCCGCTGGAATGGG 516
DB 373 GTTCTGTGCAAGTGTGTGAAACTTAATTAAGCAGACAGGACATCCGCTGGAATGGG 432
QY 517 CTGGGGGCTGACCATGCAAGAAAGTCCGAGGCACTGGCTTCTGTTAGTCAATGATA 576

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| Oy | | 577 | TGCTTTGGCCATCCTGGAACTGCTAAAGTATCACAGAAGGCTGTACAATTGACATG | 636 |
| Df | | 493 | TGCTTTGGCCATCCTGGAACTGCTAAAGTATCACAGAAGGCTGTACAATTGACATG | 552 |
| Oy | | 637 | ATATTACCATGTGTACCGCGCTGGAAAGGCTTTACACCAGGACCGGGTCATGACTG | 696 |
| Df | | 553 | ATATTACCATGTGTACCGCGCTGGAAAGGCTTTACACCAGGACCGGGTCATGACTG | 612 |
| Oy | | 697 | TGCTCTTTCATPAAGTAGAGAGTACTTCCCAGGAAGTGAGGAGCCTACGGGATACCGGAG | 756 |
| Df | | 613 | TGCTCTTTCATPAAGTAGAGAGTACTTCCCAGGAAGTGAGGAGCCTACGGGATACCGGAG | 672 |
| Oy | | 757 | CTGGCAAAGACAAAGTATTTATGCTGTAACTAACCCGCTCCGAGACGGGATGATGACGAGT | 816 |
| Df | | 673 | CTGGCAAAGACAAAGTATTTATGCTGTAACTAACCCGCTCCGAGACGGGATGATGACGAGT | 732 |
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| Oy | | 936 | CTATCTATCAAAAGACACAGCCCAAGTGTG--TGAAATTTGTCAAGAGCTTTAACTGCTTA | 993 |
| Df | | 853 | CTAATCTATCAAAAGACACAGCCCAAGTGTGAAATTTGTCAAGAGCTTTAACTGCTTA | 912 |
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| Oy | | 1050 | TATGAGACAGCTGTGGCCC | 1068 |
| Df | | 973 | TATGAGACAGCTGTGGGCC | 991 |
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| LOCUS | | | | |
| DEFINITION | | | | |
| AGENCOURT_8485556 NIH_MGC_99 Homo sapiens cDNA clone IMAGE:6305494 | | | | |
| 5', mRNA sequence. | | | | |
| BQ642872 | | | | |
| BO642872.1 GI:21767044 | | | | |
| EST. | | | | |
| SOURCE | | | | |
| ORGANISM | | | | |
| Homo sapiens (human) | | | | |
| Homosapiens | | | | |
| Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; | | | | |
| Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. | | | | |
| 1 (bases 1 to 897) | | | | |
| NIH-MGC http://mgs.nci.nih.gov/ | | | | |
| National Institutes of Health, Mammalian Gene Collection (MGC) | | | | |
| Unpublished | | | | |
| Contact: Robert Strausberg, Ph.D. | | | | |
| Email: cgapbs-r@mail.nih.gov | | | | |
| Tissue Procurement: Lou Staudt | | | | |
| cDNA Library Preparation: Rubin Laboratory | | | | |
| cDNA Library Arrayed By: The I.M.A.G.E. Consortium (ILNL) | | | | |
| DNA Sequencing by: Agencourt Bioscience Corporation | | | | |
| Clone distribution: MGC clone distribution information can be | | | | |
| found through the I.M.A.G.E. Consortium/ILNL at: | | | | |
| http://image.llnl.gov | | | | |
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QY 1261 TTCTTGAGAGACGGCCATCCCTGAGAGAGTGG-CGATGAGAGACGAGACGACCTTGA 1315

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RESULT 14
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DEFINITION AL541430 Homo sapiens PLACENTA Homo sapiens cDNA clone CS0DE006YL03
5-PRIME, mRNA sequence.
ACCESSION AL541430
VERSION AL541430.2 GI:30545601
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 1201)
Li, W.B., Gruber, C., Jesse, J., and Polayes, D.
Full-length cDNA libraries and normalization
Unpublished
On Feb 15, 2001 this sequence version replaced gi:12872494.
COMMENT Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Library: segrefgenoscope.cns.fr, Web: www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 884.f For
more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CS0DE006CF020P1&cluster=884.f. Contact :
Feng Liang Email: fliang@lifeotech.com URL :
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Library was not normalized."

BASE COUNT 294 a 250 c 312 g 284 t 61 others

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VERSION AL559849.2 GI:31283980
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ORGANISM Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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REFERENCE 1 (bases 1 to 1201)
Li, W.B., Gruber, C., Jesse, J., and Polayes, D.
Full-length cDNA libraries and normalization
Unpublished
On Feb 15, 2001 this sequence version replaced gi:12905737.
COMMENT Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Library: segrefgenoscope.cns.fr, Web: www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 884.f For
more information about this cluster, see
http://www.genoscope.cns.fr/

cg1-bin/cluster.cgi?seq=CS0DG005AD110P1&cluster=884.f. Contact :
Feng Liang Email : fliang@life.technet.com URL :
http://fulllength.livestrong.com/ InVivoGen Corporation 1600
Faraday Avenue Genoscope sequence ID : CS0DG005AD110P1.
Location/Qualifiers

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the Not I and EcoRV sites of the pCMVSPORT 6 vector.
Library was not normalized."

BASE COUNT 323 a 263 c 322 g 263 t 30 others
ORIGIN

Query Match 53.2% Score 857.4; DB 9; Length 1201;
Best Local Similarity 97.5% Pred. No. 1.6e-139;

Matches 910; Conservative 3; Mismatches 14; Indels 6; Gaps 4;

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GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 5, 2003, 13:55:37 ; Search time 122 Seconds

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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 569978 seqs, 220691566 residues

Total number of hits satisfying chosen parameters: 1139956

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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| 37 | 44.2 | 2.7 | 1926 | 4 | US-09-249-585A-4 | Sequence 4, Appl |
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ALIGNMENTS

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; Sequence 2, Application US/08528255A
; Patent No. 5659016
; GENERAL INFORMATION:
; APPLICANT: NAKAMURA, YUSUKE
; APPLICANT: FORUKAWA, YOICHI
; TITLE OF INVENTION: RPDL PROTEIN AND DNA
; TITLE OF INVENTION: ENCODING THE SAME
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESS: FLYNN, THIEL, BOUTELL & TANIS, P.C.
; STREET: 2026 Rambling Road
; CITY: Kalamazoo
; STATE: Michigan
; COUNTRY: USA
; ZIP: 49008-1699
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inches, 1.44 Mb storage
; COMPUTER: IBM PC/XT/AT Compatible
; OPERATING SYSTEM: MS-DOS 5.0
; SOFTWARE: Wordperfect 5.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/528,255A
; FILING DATE: September 14, 1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP6-227876
; FILING DATE: 22-SEPTEMBER-1994
; APPLICATION NUMBER: JP7-183763
; FILING DATE: 20-JULY-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Teruyance F. Chapman
; REGISTRATION NUMBER: 32549
; REFERENCE/DOCKET NUMBER: Futuya Case 1335
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (616) 381-1156
; TELEFAX: (616) 381-5465
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2111
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; TOPOLOGY: linear
; MOLECULE TYPE: cDNA to mRNA
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
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; LIBRARY: human fetal lung cDNA library
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NAME/KEY: CDS
 LOCATION: 64..1512
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 US-08-528-255A-2

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RESULT 2
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 Patent No. 5763182
 GENERAL INFORMATION:
 APPLICANT: NAKAMURA, YUSUKE
 TITLE OF INVENTION: RPDL PROTEIN AND DNA
 TITLE OF INVENTION: ENCODING THE SAME
 NUMBER OF SEQUENCES: 2
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: FLYNN, THIEL, BOUTELL & TANIS, P.C.
 STREET: 2026 Rambling Road
 City: Kalamazoo
 STATE: Michigan
 COUNTRY: USA
 ZIP: 49008-1699
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette, 3.5 inches, 1.44 Mb storage
 COMPUTER: IBM PC/XT/AT Compatible
 OPERATING SYSTEM: MS-DOS 5.0
 SOFTWARE: Wordperfect 5.0
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/717,365
 FILING DATE: 23-SEP-1996
 CLASSIFICATION: 536
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/528 255
 FILING DATE: September 14, 1995
 APPLICATION NUMBER: JPE-227876
 FILING DATE: 22-SEPTEMBER-1994
 APPLICATION NUMBER: JPE-183763

FILING DATE: 20-JULY-1995
ATTORNEY/AGENT INFORMATION:
NAME: Terrylene F. Chapman
REGISTRATION NUMBER: 32549
REFERENCE/DOCKET NUMBER: Furuya Case 1335
TELECOMMUNICATION INFORMATION:
TELEPHONE: (616) 381-1156
TELEFAX: (616) 381-5465
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 2111
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
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ORIGINAL SOURCE:
ORGANISM: Homo sapiens
IMMEDIATE SOURCE:
LIBRARY: human fetal lung cDNA library
FEATURE:
NAME/KEY: CDS
LOCATION: 64..1512
IDENTIFICATION METHOD: experimental examination
US-08-717-365-2

Query Match 93.0%; Score 1498; DB 1; Length 2111;
Best Local Similarity 99.3%; Pred. No. 0;
Matches 1504; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

97 GGGAGCGAGCAAGATGGCGCAGACGAGGCGACCCGAGAGAAAGTCTGTACTACTAGC 156
50 GGGAGCGAGCAAGATGGCGCAGACGAGGCGACCCGAGAGAAAGTCTGTACTACTAGC 109
157 ACGGGAGTGTGGAATTTACTATTATGAGCAAGGCCCAATGAAAGCTCACCGAATCC 216
110 ACGGGAGTGTGGAATTTACTATTATGAGCAAGGCCCAATGAAAGCTCACCGAATCC 169
217 GCGTGAATATTTGCTGCTCACTATGCTCTTACCGAAGAAATGAAATCTATCGGC 276
170 GCGTGAATATTTGCTGCTCACTATGCTCTTACCGAAGAAATGAAATCTATCGGC 229
277 CTCACAAGCGCAATGCTGAGAGATGACCAAGTACACAGCGATGACTAATTAAATTC 336
230 CTCACAAGCGCAATGCTGAGAGATGACCAAGTACACAGCGATGACTAATTAAATTC 289
337 TCGGCTTCATCGCTCAAGATACATGTCGAGTACAGCAAGCAAGTACAGATTCACG 396
290 TCGGCTTCATCGCTCAAGATACATGTCGAGTACAGCAAGCAAGTACAGATTCACG 349
397 TTGGTAGAGACTGTCAGATTTGATGAGGCTGTTGAGTCTGTCAGTTCTACTGCTG 456
350 TTGGTAGAGACTGTCAGATTTGATGAGGCTGTTGAGTCTGTCAGTTCTACTGCTG 409
457 GTTCTGTGCAAGTGTGTGAACTTAATTAAGCAGAGACGACATCGCCGTGAATGGG 516
410 GTTCTGTGCAAGTGTGTGAACTTAATTAAGCAGAGACGACATCGCCGTGAATGGG 469
517 CTGGGGGCTGCAACATGCAAGAAGTCCGAGGCATCTGCTTCTGTTACGTCAATGATA 576
470 CTGGGGGCTGCAACATGCAAGAAGTCCGAGGCATCTGCTTCTGTTACGTCAATGATA 529
577 TCGTCTTGGCATCTCGGAACTGTAAAGTATCAACAGAGGGGTGCTGTAATGACATTG 636
530 TCGTCTTGGCATCTCGGAACTGTAAAGTATCAACAGAGGGGTGCTGTAATGACATTG 589
637 ATATTACCATGTGTGACGGCGTGAAGAGGCTTCTTACACACAGGACCGGGTATGACTG 696
590 ATATTACCATGTGTGACGGCGTGAAGAGGCTTCTTACACACAGGACCGGGTATGACTG 649
697 TGTCTTTCTTAAGATGAGAGTACTTCCAGAGAACTGGGAACTTACGGGAATACCGGGG 756
650 TGTCTTTCTTAAGATGAGAGTACTTCCAGAGAACTGGGAACTTACGGGAATACCGGGG 709

QY 757 CTGGCAAGACAGATTAATGCTGTTAACTACCCGCTCCGAGACGGGATGTATGACAGT 816
DB 710 CTGGCAAGACAGATTAATGCTGTTAACTACCCGCTCCGAGACGGGATGTATGACAGT 769
QY 817 CCTATGAGGCAATTTTCAAGCCGCTCATGTCCAAAGTATGAGATGTTCCAGCTTAGT 876
DB 770 CCTATGAGGCAATTTTCAAGCCGCTCATGTCCAAAGTATGAGATGTTCCAGCTTAGT 829
QY 877 CGGTGCTTACAGTGTGCTCAGACTCCCTATCTGGGATCGGTAGGTGCTTCAATC 936
DB 830 CGGTGCTTACAGTGTGCTCAGACTCCCTATCTGGGATCGGTAGGTGCTTCAATC 889
QY 937 TATCTATCAAGACACACGCAAGTGTGAAATTTGTCAAGACTTTAACTGCTATG 996
DB 890 TAACTATCAAGACACACGCAAGTGTGAAATTTGTCAAGACTTTAACTGCTATG 949
QY 997 TGAATGCTGGAGGCGGTGTGTTACCATTTCTTACGTTGCTCCGCTGCTGACATAGAA 1056
DB 950 TGAATGCTGGAGGCGGTGTGTTACCATTTCTTACGTTGCTCCGCTGCTGACATAGAA 1009
QY 1057 CAGCTGTGGCCCTGATAGAGATATCCCTAATGAGCTTCAATACATGACTTTGAAT 1116
DB 1010 CAGCTGTGGCCCTGATAGAGATATCCCTAATGAGCTTCAATACATGACTTTGAAT 1069
QY 1117 ACTTTGACCAAGATTTCAAGCTTCAATCATGCTCTTCAATATGACTTAACAGAACGA 1176
DB 1070 ACTTTGACCAAGATTTCAAGCTTCAATCATGCTCTTCAATATGACTTAACAGAACGA 1129
QY 1177 ATGAGTACTGTGAGAAAGATCAACAGCGACTGTTTGAAGAACTTGAATGCTGCGCAG 1236
DB 1130 ATGAGTACTGTGAGAAAGATCAACAGCGACTGTTTGAAGAACTTGAATGCTGCGCAG 1189
QY 1237 CAGCTGGGTCCAAACGCAAGGCGATTCCTGAGAGCGCCATCCCTGAGAGAGTGGGATG 1296
DB 1190 CAGCTGGGTCCAAACGCAAGGCGATTCCTGAGAGCGCCATCCCTGAGAGAGTGGGATG 1249
QY 1297 AGGACGAGACGACCTGTAACAAGCGATCTGATGCTGCTCTGTAACAAGATGGCT 1356
DB 1250 AGGACGAGACGACCTGTAACAAGCGATCTGATGCTGCTCTGTAACAAGATGGCT 1309
QY 1357 GTGAGGAGAGTCTTCCGATTTCTGAAGAGAGGAGGCGCGCAAGATCTTCC 1416
DB 1310 GTGAGGAGAGTCTTCCGATTTCTGAAGAGAGGAGGCGCGCAAGATCTTCC 1369
QY 1417 ACTTCAAAAAAGCCAAAGAGTCAAAAACAGAGATTAATAAGAAAGCCCAAGAGAG 1476
DB 1370 ACTTCAAAAAAGCCAAAGAGTCAAAAACAGAGATTAATAAGAAAGCCCAAGAGAG 1429
QY 1477 AGAAGAGATCAACCGAAGAGAGAGAAACCAAGAGAGAGCAAGAGCCAAAGGGGTCA 1536
DB 1430 AGAAGAGATCAACCGAAGAGAGAGAAACCAAGAGAGAGCAAGAGCCAAAGGGGTCA 1489
QY 1537 AGGAGAGGCAAGTGTGCTGAAATGACCTTCCAGCTTGTGCTTCTGCTGATGCTT 1596
DB 1490 AGGAGAGGCAAGTGTGCTGAAATGACCTTCCAGCTTGTGCTTCTGCTGATGCTT 1549
QY 1597 CACGTTCTTTCC 1610
DB 1550 CACGTTCTTTCC 1563

RESULT 3
US-09-282-305-7
Sequence 7, Application US/09282305
Patent No. 6287843
GENERAL INFORMATION:
APPLICANT: Baldwin, Donald A.
APPLICANT: Briggs, Steven P.
APPLICANT: Crane, Virginia C.
TITLE OF INVENTION: Maize Histone Deacetylases And Their Uses
FILE REFERENCE: 5718-44,
CURRENT APPLICATION NUMBER: US/09/282,305
CURRENT FILING DATE: 1999-03-31

PRIOR APPLICATION NUMBER: 60/080,563
 PRIOR FILING DATE: 1998-04-03
 NUMBER OF SEQ ID NOS: 18
 SOFTWARE: Patentln Ver. 2.0
 SEQ ID NO: 7
 LENGTH: 1943
 TYPE: DNA
 ORGANISM: Zea mays
 FEATURE:
 NAME/KEY: CDS
 LOCATION: (57)..(1610)
 US-09-282-305-7

Query Match 31.2%; Score 502.6; DB 3; Length 1943;
 Best Local Similarity 65.5%; Pred. No. 3,5e-143;
 Matches 768; Conservative 0; Mismatches 399; Indels 6; Gaps 2;

| | | | |
|----|-----|--|-----|
| Qy | 134 | GAGGAAAGCTCTTACTTACGACGCGGAGTGTGGAATTACTATTATGACAAAGGCCA | 193 |
| Db | 122 | GCGGCGGTGTGTTACTTCTACGACCGGATGTGGGCAACTACTATACGGGAGGGCCA | 181 |
| Qy | 194 | CCCAATGAAGCTCAACGGAATCCGCAATGACTATATTGTGCTCAACTATGTCTCTA | 253 |
| Db | 182 | TCCGATGAAGCCGACCGCATCCGATGACGACTCGCTGCGGCGCTACGGCTCTCT | 241 |
| Qy | 254 | CCGAAAATGGAATCTATCGCCCTCAACAAGCCCAATGCTGAGAGATGACCAAGTACA | 313 |
| Db | 242 | CAACCAATGACAGGTGTACCGCCCAACCGGCGCGGACCGGACCTCTGCGCTTCCA | 301 |
| Qy | 314 | CAGCGATGACTACTTAATTTCTTGCGCTCCATCCGTCCAGATTAACATGTGAGTACAG | 373 |
| Db | 302 | CGCGGACGACTACATCAACTTCTGCGCTCCGTACCGCGGAAACGACGAGACAGAT | 361 |
| Qy | 374 | CAACGATGACGAGATTCACGTTGGGAGAGACTGTCCAGATTTCCATGGCCCTGTGA | 433 |
| Db | 362 | CCGCTGTCAAGCGCTTCAACGTCGCGGAGAGACTGCCCCCTTCCAGCGGCTTACAG | 421 |
| Qy | 434 | GTTCTGTCAAGTGTCTACTGCTGCTGTGGCAAGTCTGTGAACCTTAATTAAGACGA | 493 |
| Db | 422 | CTTCTGCAAGACTATGCGGCGGCTCCGTGCGGCGGCGCTCAAGCTCAACGACGCGCA | 481 |
| Qy | 494 | GACGACATCGCCGTGAATTGGGCTGGGGCTTCGACCAATGCAAAAGATCCGAGGATC | 553 |
| Db | 482 | ---TGACATCGCAATCAACTGCTGGGGGGCTCGACACCAAGATCCGAGGCTC | 538 |
| Qy | 554 | TGCTTCTGTACGTCATGATATGCTTGGCCATCTGTGAATGCTGAAGTATACCA | 613 |
| Db | 539 | GCGCTTCTGCTACGTCATGATGATGCTGCTGCACTCGAGCTGCTCAAGCATCACA | 598 |
| Qy | 614 | GAGGATGCTGTACATGATGATTAATTCACCATGCTGACCGCGTGAAGAGGCTTCTA | 673 |
| Db | 599 | GAGGATGCTGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT | 658 |
| Qy | 674 | CACCAAGGACCGGCTCATGATGCTGTCTTTCATTAAGTATGAGAGTACTTCCAGAAC | 733 |
| Db | 659 | CACAACAGATGAGGCTATGATGCTGTCTTTCACAAGTATGATTAATTTCCAGAAC | 718 |
| Qy | 734 | TGGGACCTTACGGAATACCGGCGCTGGAAGACAAAGTATATGCTGTAACTACCGCT | 793 |
| Db | 719 | AGGGATATTCGTATCATTTGGGCACTCAAAAGGAGTACTCTCCCTGAATGTCTCT | 778 |
| Qy | 794 | CCGAAAGGAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT | 853 |
| Db | 779 | AGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT | 838 |
| Qy | 854 | AATGAGATGTTTCAAGCTTACGCTGCTTCAAGTGTCTTCAAGTGTCTTCAAGTGTCT | 913 |
| Db | 839 | TATGAGATGTTTCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT | 898 |
| Qy | 914 | GATGCTGTTAGTGTCTTCAATCTATCTATCAAAAGACACCCCAAGTGTGTGAATTTGT | 973 |
| Db | 899 | GGATGATGTTGGCTGCTTCAACTCTCAATCAAAAGTGTGTGTGTGTGTGTGTGTGT | 958 |

| | | | |
|----|------|--|------|
| Qy | 974 | CAAGGCTTTAACTGCTGCTGATGCTGGAGCGGTGTGTATACCAATTCGTACGT | 1033 |
| Db | 959 | GAGGCTTTAAAGTGTCAATGTTGTGCTTGTGATGATGATGATGATGATGATGATGAT | 1018 |
| Qy | 1034 | TGCGGCTGTGACATATGACAGCTGTGCGCTGTGATACGAGATTCCTTAATGAGCT | 1093 |
| Db | 1019 | TGCAAGCTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT | 1078 |
| Qy | 1094 | TCCATCAATGACTACTTGAATATCTTTGACAGATTTCAAGTCTCACATGAGTCTTC | 1153 |
| Db | 1079 | GCTGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT | 1138 |
| Qy | 1154 | CAATGACTTACAGACAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT | 1213 |
| Db | 1139 | TAACTGAGACAAATAATACAGACAACTGATGATGATGATGATGATGATGATGATGAT | 1198 |
| Qy | 1214 | GAACTTGAATGCTGCGGACGACCTGGGGTTCAAACGAGCGA---TTCTGAGGA | 1270 |
| Db | 1199 | TAACTTTCAAACTTCGACATGCTCTTACTGTTCATTTCAGAGAGAGATTCCTGAC | 1258 |
| Qy | 1271 | CGCATCCCTGAGAGAGTGGCATGAGACGA | 1303 |
| Db | 1259 | AGAAATCTTGACGAGATGAAATCAAGTGA | 1291 |

RESULT 4

US-09-883-720-7

Sequence 7, Application US/09883720
 Patent No. 6479629
 GENERAL INFORMATION:
 APPLICANT: Baldwin, Donald A.
 APPLICANT: Bridger, Steven P.
 APPLICANT: Crane, Virginia C.
 TITLE OR INVENTION: Maize Histone Deacetylases And Their Uses
 FILE REFERENCE: 5718-44,
 CURRENT APPLICATION NUMBER: US/09/883,720
 PRIOR FILING DATE: 2001-06-18
 PRIOR FILING DATE: 1999-03-31
 NUMBER OF SEQ ID NOS: 18
 SOFTWARE: Patentln Ver. 2.0
 SEQ ID NO: 7
 LENGTH: 1943
 TYPE: DNA
 ORGANISM: Zea mays
 FEATURE:
 NAME/KEY: CDS
 LOCATION: (57)..(1610)
 US-09-883-720-7

Query Match 31.2%; Score 502.6; DB 4; Length 1943;
 Best Local Similarity 65.5%; Pred. No. 3,5e-143;
 Matches 768; Conservative 0; Mismatches 399; Indels 6; Gaps 2;

| | | | |
|----|-----|--|-----|
| Qy | 134 | GAGGAAAGCTCTTACTTACGACGCGGAGTGTGGAATTACTATTATGACAAAGGCCA | 193 |
| Db | 122 | GCGGCGGTGTGTTACTTACGACCGGATGTGGGCAACTACTATACGGGAGGGCCA | 181 |
| Qy | 194 | CCCAATGAAGCTCAACGGAATCCGCAATGACTATATTGTGCTCAACTATGCTCTA | 253 |
| Db | 182 | TCCGATGAAGCCGACCGCATCCGATGACGACTCGCTCGCGGCTACAGGCTCTCT | 241 |
| Qy | 254 | CCGAAAATGGAATCTATCGCCCTCAACAAGCCCAATGCTGAGAGATGACCAAGTACA | 313 |
| Db | 242 | CAACCAATGACAGGTGTACCGCCCAACCGGCGCGGACCGGACCTCTGCGCTTCCA | 301 |
| Qy | 314 | CAGCGATGACTACTTAATTTCTTGCGCTCCATCCGTCCAGATTAACATGTGAGTACAG | 373 |
| Db | 302 | CGCGGACGACTACATCAACTTCTGCGCTCCGTACGCGGAAACGACGAGACAGAT | 361 |
| Qy | 374 | CAACGATGACGAGATTCACGTTGGTGAAGACTGTCAGTATTTGATGATGCTGTTGA | 433 |
| Db | 362 | CCGCTGTCAAGCGCTTCAACGTCGCGGAGAGACTGCCCCGTCTTCAAGCGGCTTACAG | 421 |

QY 434 GTTCTCTAGTGTCTACTGTTGTTCTGTGCGAAGTGTGTAATTAATAGACA 493
 DB 422 CTTCTCCAGACCTATGCGGGGCGCTTCGCGGGGGGCGCTCAAGCTCAACGACCA 481
 QY 494 GACGACATCGCCGTAATTGGCTGGGGGCTGCAACCATGCAAGAAGTCCGAGGATC 553
 DB 482 ---TGACATCGCAATCAATGCTGGGGGGGCTGCAACGCGCAAGAAGTGGAGGCTC 538
 QY 554 TGGCTCTGTAGTCAATGATATGCTCTGGCCATCTGGAACTGCTAAAGTATACCA 613
 DB 539 GGGCTCTGTAGTCAATGATATGCTCTGGCCATCTGGAACTGCTAAAGTATACCA 598
 QY 614 GAGGGTCTGTAGTCAATGATATGCTCTGGCCATCTGGAACTGCTAAAGTATACCA 673
 DB 599 GAGAGTCTGTAGTCAATGATATGCTCTGGCCATCTGGAACTGCTAAAGTATACCA 658
 QY 674 CACACAGACCGGGTATGATGCTGTCTTCAATGATGAGAGTACTTCCAGGAA 733
 DB 659 CACACAGATAGGGTATGATGCTGTCTTCAATGATGAGAGTACTTCCAGGAA 718
 QY 734 TGGGACCTACCGGATACCGGGGCTGGCAAGCAAGTATATGCTGTACTACCCGCT 793
 DB 719 AGGGATATCCGATGATGAGGCACTCAAAAGGAAAGTACTCTCCCTGATGCTCT 778
 QY 794 CCGAGACGGGATGATGACGATGCTATGAGGCACTTTCAGCCGGTATGCAAGT 853
 DB 779 AGATGATGGGATGATGATGAGGCACTCAAAAGGAAAGTACTCTCCCTGATGCTCT 838
 QY 854 AATGAGATGCTTCAAGCTATGAGGCTGTCTTCAAGTGTGCTCAAGTCTCTATCTG 913
 DB 839 TATGAGGATTTCCGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 898
 QY 914 GATGCTGTAGTGTCTTCAATGATGATGATGATGATGATGATGATGATGATGAT 973
 DB 899 GATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 958
 QY 974 CAGAGCTTAACTGCTATGCTGATGCTGATGCTGATGCTGATGCTGATGCTGAT 1033
 DB 959 GAGGCTTTCAGCTTCCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1018
 QY 1034 TGGCCGCTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1093
 DB 1019 TGGACGCTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1078
 QY 1094 TCCATCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1153
 DB 1079 GCTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1138
 QY 1154 CATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1213
 DB 1139 TAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1198
 QY 1214 GAACCTTAAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1270
 DB 1199 TATCTTTGAAATCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 1258
 QY 1271 CGCCATCTGTGAGAGAGTGGCATGAGACA 1303
 DB 1259 AGAATATCTGAGCAAGATGATGATGATGATGATGATGATGATGATGATGATGAT 1291

RESULT 5
 US-09-282-305-5
 ; Sequence 5, Application US/09282305
 ; Patent No. 6287843
 ; GENERAL INFORMATION:
 ; APPLICANT: Baldwin, Donald A.
 ; APPLICANT: Briggs, Steven P.
 ; APPLICANT: Crane, Virginia C.
 ; TITLE OF INVENTION: Maize Histone Deacetylases And Their Uses
 ; FILE REFERENCE: 5718-44,
 ; CURRENT APPLICATION NUMBER: US/09/282,305

; CURRENT FILING DATE: 1999-03-31
 ; PRIOR APPLICATION NUMBER: 60/080,563
 ; PRIOR FILING DATE: 1998-04-03
 ; NUMBER OF SEQ ID NOS: 18
 ; SOFTWARE: Patentin Ver. 2.0
 ; SEQ ID NO 5
 ; LENGTH: 2019
 ; TYPE: DNA
 ; ORGANISM: Zea mays
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: (140) .. (1459)
 ; US-09-282-305-5
 Query Match 31.1%; Score 501.8; DB 3; Length 2019;
 Best Local Similarity 65.3%; Pred. No. 6.3e-143;
 Matches 753; Conservative 0; Mismatches 397; Indels 3; Gaps 1;
 QY 121 CCGAGGACACCGGAGGAAGTCTGTACTACGACGGGAGTGTGAAATTAATTA 180
 DB 189 CGGAGGATGAAAGCGCGGCTGTCTACTTCTACGACGGGAGTGGCACTACT 248
 QY 181 ATGACACAGGCCAATGAAAGCTTACCGAATCCGATGACTCAATTTGCTCTCA 240
 DB 249 ACGGGCAGGGCCACCGATGAAAGCCGATCCGATCCGATCCGATCCGCTGGCC 308
 QY 241 ACTATGCTTCAACGAAATGAAATGAAATGAAATGAAATGAAATGAAATGAAAT 300
 DB 309 GCTACGGCTCTCTGACGATGCAAGTGTCCGCTCAACCTGCGCGACCGGACC 368
 QY 301 TGACCAATGACACGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 360
 DB 369 TCTGCGCTTCCACGCGGACGATGATGATGATGATGATGATGATGATGATGATGAT 428
 QY 361 TGTGGAGTACGACGACGATGACGATGACGATGACGATGACGATGACGATGACGAT 420
 DB 429 AGCAGACCAAGATCCGCGGCTCAAGCGCTTCAAGCGGCGAGGACCTCCGCTT 488
 QY 421 ATGCGCTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 480
 DB 489 ACGGCTCTCAAGTTCGTGACGATGACGATGACGATGACGATGACGATGACGATGAC 548
 QY 481 TTAATGACGACGACGATGACGATGACGATGACGATGACGATGACGATGACGATGAC 540
 DB 549 TCAACCATGACCA---TGATATGCGCATCACTGGCGGCGGATCCACGACCAAGA 605
 QY 541 AGTCGAGGCACTGTGCTTCTGTATGCTGATGATGATGATGATGATGATGATGATGAT 600
 DB 606 AGTGGAGGCTCCGGGTTTGTGATGATGATGATGATGATGATGATGATGATGATGAT 665
 QY 601 TAAATGATGACGAGGCTGTGATGATGATGATGATGATGATGATGATGATGATGAT 660
 DB 666 TCAAGTACCAACGACGCTTCTGTGATGATGATGATGATGATGATGATGATGATGAT 725
 QY 661 AAGAGGCTTCAACGACGACGCGGATGATGATGATGATGATGATGATGATGATGATGAT 720
 DB 726 AGAGGCTTTCATGACGACGCGGATGATGATGATGATGATGATGATGATGATGATGAT 785
 QY 721 ACTTCCAGGAATGAGGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 780
 DB 786 ATTTCCCTGGGACAGGGAATTCGATGATGATGATGATGATGATGATGATGATGATGAT 845
 QY 781 TTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 840
 DB 846 TGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 905
 QY 841 TCAATGCAAGGAATGAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 900
 DB 906 TAAATGACGAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 965
 QY 901 ACTCCCTATCTGGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 960
 DB 966 ATTCAATGCTGGGTGACAGGTTGGGCTTTCAACCTCTATTAAGGCTCAGCAGAA 1025

CURRENT APPLICATION NUMBER: US/09/282,305
CURRENT FILING DATE: 1999-03-31
PRIOR APPLICATION NUMBER: 60/080,563
PRIOR FILING DATE: 1998-04-03
NUMBER OF SEQ ID NOS: 18
SOFTWARE: Patent Ver. 2.0
SEQ ID NO 9
LENGTH: 1576
TYPE: DNA
ORGANISM: Zea mays
FEATURE:
NAME/KEY: CDS
LOCATION: (38) .. (1336)
US-09-282-305-9

Query Match 28.6%; Score 460.8; DB 3; Length 1576;
Best Local Similarity 62.0%; Pred. No. 1,8e-130;
Matches 764; Conservative 0; Mismatches 462; Indels 6; Gaps 2;

159 GGGAGTGTGGAATACTATTATGAGCAAGGCCACCATGAAAGCCTCAGCCATCCGC 218
80 GGGAGTGTGGAATACTATTATGAGCAAGGCCACCATGAAAGCCTCAGCCATCCGC 139
219 ATGACTCATATTTGCTGCTCAACTATGCTCTACCGAAAAATGAAATCTATCCCTT 278
140 ATGACATCATCTGTTCTTTTATATGACCTTCATCAAAAGATGAGATATAGGCCA 199
279 CACAAAGCCATGCTGAGAGATGACCAAGTACCAAGGATGATCATTAATTTCTTG 338
200 CACAAAGCATATCCAAATAGAGCTTGCCTCATTTCTGCTATTAATGGAATTTCTTG 259
339 CGCTCATCCGTCAGATTAACATGTCGAGATACAGCAAGCAAGATGAGATTCACGTT 398
260 CACCGATATCTCTGATTCACGACCTATATGCAAGTAACTAATGATCAATCTT 319
399 GGTGAGACTGTCAGATTTGATGAGCTGTTGAGTTCTGCTGATGCTGATGCTGCT 458
320 GAGAGAGCTGTCGGGCTTTGATTAATTTGTTGAGTTCTGCCAAATCTATGCGGAGGA 379
459 TCTGTGCAAGTCTGTAAGCTTAATAGCAGACAGCAAGCATCCCGTGAATGGCT 518
380 ACTTTAGATGCTGCTGCGAGATTAATCATTAATATGTCACATTCGCTATTAATGGGCT 439
519 GGGGCTGCTGACCATGAAAGAGTCCGAGGCTGCTGCTGATACGATGATGATC 578
440 GGTGAGCTATCATATGCAAAAGTGTGAGGCTTCAAGCTTCTGATCAATTAATGATCTA 499
579 GTCCTGAGCATCTGGAATGCTTAAGTATCACAGAGGCTGCTGATCAATTCATTCAT 638
500 GTATTGGAATTTGAGGCTTCTCAAGTACCAAGGCTTCTTATTAATTCATTCATTCAT 559
639 ATTACCATGATGAGCGGCTGGAAGAGGCTTCTCAACAGCGAGCGGCTGATGCTG 698
560 GTCCATCATGAGATGAGATGAAGGCTTTTATTTTCACTGACAGGGTAAATGAGCTG 619
699 TCCCTTCAATAGATGAGA---GTACTTCCAGAGAACTGGGAGCTTACCGGATACCGG 755
620 AGTTTCCACAAGATGATGAGCTGTTCTTTCGGAACAGGTATTAAGATATAGGA 679
756 GCTGCAAAAGACAGTATTAAGCTGTTTAACTACCCGCTCCGAGACGGGATTTGATGAG 815
680 GAAAGGAGGAAATTTATTTGCTATCAATTCCTTAAAGATGAGATGATGACAT 739
816 TCTTATGAGGCAATTTTCAAGCCGCTGATGTCAGAAAGTAAATGAGATGTTTCAAGCT 875
740 AGCTTATCTGCGCTTTTAAACAATATTCAGAAAGTGTGAGACATATTCGCTGAT 799
876 GCGGTGCTTAAAGTGTGCTGAGATCCCTATCTGGGATGCGTAAAGTGTGCTTCAAT 935
800 GCTATGTTCTTCAATGTTGGGCTGATTCATGCGAGGATGCTTTAAGGCTGCTCAAT 859
936 CTATCTATCAAGAGACAGCGCAAGTGTGGAATTTGTCAAGAGCTTAACTGCTCATG 995

860 CTCTTATGGAAGCCAGCTGATATGTTGAAGTTTGCAGAAATTCATATTCCTT 919
996 CTGATGCTGAGAGGGGCTGTTTACCAATTCCTTAAAGTTGCGGCTGCTGACATATGAG 1055
920 CTGTATCTGAGAGTGTGATGATACCAAGAGAAATGATGACAGGCTGTTGAA 979
1056 ACAAGCTGTGGCCCTGATACGAGATTCCTTAATGAGCTTCCATACATGATCTTGA 1115
980 ACTGGGCTCTTTTATGACACAGACTCCCAATATGAGATTCAAAAATATATATTTAG 1039
1116 TACTTGAACCAATTTCAAGCTTCAATCAATCTCTTCAATATGATCAACAGCAAG 1175
1040 TACTTGTCTCCAGATTAATCAATGAAGTTCCAAATTTGAACATGATTTGAACAGT 1099
1176 AATGATACCTCGAGAGATCAACAGCAAGCTTGTGAGACCTTGAATGCTGCGCAC 1235
1100 AAGACTATCTCAATTCATCAATCAAGTGAAGTGAAGATTTGGGATCATACAGCAT 1159
1236 GCACTGGGCTCCAAACGAGGCGATTCCTGAGAGCGCCATCCCTGAGAGAGTGGCAT 1295
1160 GCTCCTGCTTCAATGCAAGAGGTTCTCCGATTTTATATCCCGGACTTT---GAT 1216
1296 GAGAGCAAGACGACCTTGAACAGGCAATCTGATCTCTCTTCAACAAAGATTCG 1355
1217 GAAAGTAAATGATGATCTGATGAAAGCTGTTGACCAAGCACTCCAAAGCAAGATTCAC 1276
1356 TGTGAGAGAGTCTCCGATTCCTGAGAG 1387
1277 CGTATGATGATGATCTATGAGGTTGCAATGA 1308

RESULT 8

US-09-883-720-9
Sequence 9, Application US/09883720

Patent No. 6479629

GENERAL INFORMATION:

APPLICANT: Baldwin, Donald A.

APPLICANT: Briggs, Steven P.

APPLICANT: Crane, Virginia C.

TITLE OF INVENTION: Maize Histone Deacetylases And Their Uses

FILE REFERENCE: 5718-44,

CURRENT APPLICATION NUMBER: US/09/883,720

PRIOR FILING DATE: 2001-06-18

PRIOR APPLICATION NUMBER: 09/282,305

PRIOR FILING DATE: 1998-03-31

NUMBER OF SEQ ID NOS: 18

SOFTWARE: Patent Ver. 2.0

SEQ ID NO 9

LENGTH: 1576

TYPE: DNA

ORGANISM: Zea mays

FEATURE:

NAME/KEY: CDS

LOCATION: (38) .. (1336)

US-09-883-720-9

Query Match 28.6%; Score 460.8; DB 4; Length 1576;
Best Local Similarity 62.0%; Pred. No. 1,8e-130;
Matches 764; Conservative 0; Mismatches 462; Indels 6; Gaps 2;

159 GGGAGTGTGGAATACTATTATGAGCAAGGCCACCATGAAAGCCTCAGCCATCCGC 218
80 GGGAGTGTGGAATACTATTATGAGCAAGGCCACCATGAAAGCCTCAGCCATCCGC 139
219 ATGACTCATATTTGCTGCTCAACTATGCTCTACCGAAAAATGAAATCTATCCCTT 278
140 ATGACATCATCTGTTCTTTTATATGACCTTCATCAAAAGATGAGATATAGGCCA 199
279 CACAAAGCCATGCTGAGAGATGACCAAGTACCAAGGATGATCATTAATTTCTTG 338
200 CACAAAGCATATCCAAATAGAGCTTGCCTCATTTCTGCTATTAATGGAATTTCTTG 259
339 CGCTCATCCGTCAGATTAACATGTCGAGATACAGCAAGATGAGATTCACGTT 398

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Db      | 260 CACCGGTAACCTCTGATCCACGACCACTATATGCAATGCACTAATCAATCTT 319
Qy      | 399 GGTGAGAGACCTGCAAGTTCAGATGAGCGCTGTTGAGTTCGTGCTGCTACTGCTGT 458
Db      | 320 GGAGAAAGACGTGCGGCTTGTGAATATTTGTTGAGTTGCTCCAAATCTATGCGGAGGA 379
Qy      | 459 TCTGTGCAAGTGTGTGAACTTAATAGACAGACGACATCGCGTGAATTTGGCT 518
Db      | 380 ACTTATATGCTGTGTCAGATTAATCATTAATATATGATGACATGSCATTAATTTGGCT 439
Qy      | 519 GGGGGCTGCAACATGCAAAAGAGTCCGAGCATCTGCTTCTGTATCGTCATATATATC 578
Db      | 440 GGTGGCTACATCATGCAAAAGTGAAGCTTCAGGCTTCTGTATCATTAATGATCTA 499
Qy      | 579 GTCTGGCCATCTCCGAACTGCTAATATACAGAGGGGCTGTACATTAATGATGAT 638
Db      | 500 GTATTTAGAAATCTGAGCTTCTCAAGTACCATGCGAGGTTCTTTATATTTGACATTTGAT 559
Qy      | 639 ATTCAACATGATGACGCGGTGGAAGAGGCTTTACACACGACCGGTCATGATGCTG 698
Db      | 560 GTCTATATGAGATGAGATTTGAAGAGCCTTTATTTCTGACAGGATATGATCTGTG 619
Qy      | 699 TCCTTTATAAGTATGAGA---GTACTTCCAGAACTGAGGACTTACGAGATACCGGG 755
Db      | 620 AGTTTCAACAGTATGAGTACCTGTTCTTCTGGAACAGGTATTAAGATATAGGA 679
Qy      | 756 GCTGGCAAGACAGTATATGCTGTATACATCCCGCTCCGACGCGGATGATGAGAG 815
Db      | 680 GAAAGGAAAGAAATATATATGCTATCAACATTCACATTAAGATGAGATGAGACT 739
Qy      | 816 TCTATGAGGCACTTTTCAAGCCGTCATGTCACAAAGTATGAGATGTTCCAGCTAGT 875
Db      | 740 AGCTTACTCGGCTTTTAAACAATATATGCAAAAGTGTGAGACATATCTGCTGCT 799
Qy      | 876 GCGGTGCTTACAGTGTGCTCAGACTCCCTATCTGGGAGTGGTTAGTTGCTTCAAT 935
Db      | 800 GCTATTTCTTCAATGAGGCTGATGATTCATTTGCGAGGATCGTTTAAAGCTGCTCAAT 859
Qy      | 936 CTATCTTCAAGAGACGCGCAAGTGTGGAATTTGTCAGACCTTTAATCTGCTCATG 995
Db      | 860 CTCTCTATGAAAGCCATGCTGAATGTGTAAGTTTGAAGAAATTCATATATCTT 919
Qy      | 996 CTATGCTGAGAGCGGTGTTACACCATTCATGTAAGTTCGCGGTGCTGACATATGAG 1055
Db      | 920 CTGTTACTGAGGTGTGTGATACACCAAGAGATATGAGACGCTGTGCTGTTGAA 979
Qy      | 1056 ACAGCTGTGCGCTGATACGAGATCCCTATATGAGCTTCATACATGACTTCTTGA 1115
Db      | 980 ACTGGGGCTTTTGAACAGAACTCCCAATGAGATTCAAAAAATGAATATATGAG 1039
Qy      | 1116 TACTTTGACCAAGATTTCACTCAATCACTCTTCCATATATGATCAACCAACACG 1175
Db      | 1040 TACTTTGCTCCAGATTAATATGTAAGTTTCAAAATTTGAACATGACAAATTTTAAAGCT 1099
Qy      | 1176 AATGAGTACTGGAAGATCAAAACAGGACCTGTTTGAACCTTAGAATCTGCGGAC 1235
Db      | 1100 AAGACTATCTCACTGTTCAATCAAACTGCAAGTGTGAGAGATTTGCGGTATATACAGAT 1159
Qy      | 1236 GCACCTGGGGTCAAAACGACGAGATTCCTGAGGACGCGCATCCCTGAGAGAGTGGCAT 1295
Db      | 1160 GCTCTGCTGTGTTCAAAATGCAAGAGGTTCTCCGATTTTATATCCCGGACTTT---GAT 1216
Qy      | 1296 GAGACGAAAGACGACCTGACAAAGGCAATCTGATCTGCTCTCTGACAAACGAATGCC 1355
Db      | 1217 GAAGATGATTTGATCTCTGATGAACGTGTGACCAAGCACTCAAGACAAAGCAATTCAC 1276
Qy      | 1356 TGTGAGAAAGATCTCCGATTTCTGAAGAGA 1387
Db      | 1277 CGTGATGATGACTATGAAGGTGACATGA 1308

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RESULT 9

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US-09-282-305-1
; Sequence 1, Application US/09282305
; Patent No. 6287843
; GENERAL INFORMATION:
; APPLICANT: Baldwin, Donald A.
; APPLICANT: Briggs, Steven P.
; APPLICANT: Crane, Virginia C.
; TITLE OF INVENTION: Maize Histone Deacetylases And Their Uses
; FILE REFERENCE: 5718-44,
; CURRENT APPLICATION NUMBER: US/09/282,305
; PRIOR FILING DATE: 1999-03-31
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 1:
; LENGTH: 1826
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (29)..(1405)
US-09-282-305-1
Query Match      28.5%; Score 459; DB 3; Length 1826;
Best Local Similarity 61.8%; Pred. No. 7e-130;
Matches 729; Conservative 0; Mismatches 450; Indels 0; Gaps 0;
Qy      | 131 CCGAGAAAGTCTGTACTTACTTACGACGGGATGTTGAAATTTACTATATGACAAAG 190
Db      | 88 CCGCGCGCGGTAGCTATTTTACAGACCGTGAATGAGACTACTACTACGAGCAAG 147
Qy      | 191 CCACCCATGAGACCTTCAACCGAATCCGATGACTCAATTTGCTGCTCAATATGCTT 250
Db      | 148 TCACCGATGAACCCCAACCGCATCCGAATGGGCACTGCTGTGTGTCACATCGGCT 207
Qy      | 251 CTACCGAAATGAAATCTATGCTCCCTCAAAAGCCATGCTGAGAGATGACAAATGA 310
Db      | 208 CCACCGCTCTGAGGCTCCCGCCCTTACCGGCTCTGAGGCGGACATCCGCGCTT 267
Qy      | 311 CCACAGGATGACTACTTAATTTTGGCTCCATCCGTCGATTAACATGTGAGATA 370
Db      | 268 CCACCTCGAGACTAGCTGCTTCTCGCTCGCCACCGAAACCGGCTGCTTGA 327
Qy      | 371 CACGACGAGATGACAGATTTCAACGTGTGAGACTGTCCAGATATTCATGAGCTGTT 430
Db      | 328 CCGCGGCGCATTAAGGCTTTAAGTGTGAGAGTGTGCGGCTGTGAGCGGTCTT 387
Qy      | 431 TGAATCTGTCACTGTCTTACTGAGTGTGTGTGCAAGTGTGTGAATTTAATGA 490
Db      | 388 CCGCTTCTGCAAGGCTCCGCTGGGGGAAAGCATCGCGCGCTCAAGCTTAAACCGCG 447
Qy      | 491 GCAGAGGAGATGCGCTGAATTTGGGTGGGGGCTTCACATGAGAAAGTCCGAGG 550
Db      | 448 GGAAGCGGAGATCAACCTCACTGAGGCGGCGCTTCACACAGCCAAAGAGCGAGG 507
Qy      | 551 ATCTGCTTCTGTTACGTATGATATCTTGGCCATCTGGAATCTGTAAGTATCA 610
Db      | 508 CTCGAGTCTGTACGTCAACGATGTCATGTCCTTTCACAAATATGAGGATTTTCCCTGG 567
Qy      | 611 CCAAGGATCTGTACATTAATGATTAATTCACATGATGACGCGCTGGAAGAGGCTT 670
Db      | 568 CAGCGGTGCTATATATGATGACATGATGTCACCATGAGATGCGTGAAGAGGCTT 627
Qy      | 671 CTACACAGGAGCGGCTATGACTGTGCTTTCATTAATATGAGAGTACTTCCAGG 730
Db      | 628 CTTCATCAAAACGAGTCAATGACTGTTCTTTCACAAATATGAGGATTTTCCCTGG 687
Qy      | 731 AACTGGGACCTACGAGTACCGGGCTGGCAAGCAATATATATCTGTTAACTACC 790
Db      | 688 TACTGACATATACATGATGAGGCGAGCGAAGGAAACATTAATCTCTGAAATGTTCC 747
Qy      | 791 GCTCCGAGAGGATTTGATGACAGATCTATGAGGCCATTTTCAAGCGGCTCATGCCAA 850

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;; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
;; TITLE OF INVENTION: DIAGNOSIS OF BREAST CANCER
;; FILE REFERENCE: 210121.470C8
;; CURRENT APPLICATION NUMBER: US/09/620,405B
;; CURRENT FILING DATE: 2000-07-20
;; NUMBER OF SEQ ID NOS: 495
;; SOFTWARE: FastSeq for Windows Version 3.0
;; SEQ ID NO: 403
;; LENGTH: 241
;; TYPE: DNA
;; ORGANISM: Homo sapiens
;; FEATURE:
;; NAME/KEY: misc feature
;; LOCATION: (1)...(241)
;; OTHER INFORMATION: n = A,T,C or G
US-09-620-405B-403

Query Match 14.6%; Score 235.8; DB 4; Length 241;

Best Local Similarity 98.8%; Pred. No. 3.1e-62;
Matches 237; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

| | | | |
|----|-----|--|------|
| QY | 777 | GCTGTTAACTACCGGCTCCGAGACGGAGTGTATGACGAGTCCTATGAGGCCATTTCAG | 836 |
| DB | 2 | GGTGTAACTAACCGGCTCCGAGACGGAGTGTATGACGAGTCCTATGAGGCCATTTCAG | 61 |
| QY | 837 | CCGGTCATGTCCAAAGTATGAGATGTTCCAGCCTAGTGGGTGTTCTTACAGTGTGC | 896 |
| DB | 62 | CCGGTCATGTCCAAAGTATGAGATGTTCCAGCCTAGTGGGTGTTCTTACAGTGTGC | 121 |
| QY | 897 | TCAGACTCCCTATCTGGGGATCGGTTAGTTGCTTCAATCTATCTATCAAGAAGACACGCC | 956 |
| DB | 122 | TCAGACTCCCTATCTGGGGATCGGTTAGTTGCTTCAATCTATCTATCAAGAAGACACGCC | 181 |
| QY | 957 | AAGTGTGTGAATTGTCAAGAGCTTTACCTGCTATGCTGAGGAGGCGGTGT | 1016 |
| DB | 182 | AAGTGTGTGAATTGTCAAGAGCTTTACCTGCTATGCTGAGGAGGCGGTGT | 241 |

Search completed: December 5, 2003, 16:41:15
Job time : 138 secs

[illegible]

| | | | |
|----|------|--|------|
| Db | 1261 | TTCTGAGGAGCGCCATCCCTGAGAGGTGGCCATGAGGACGAAGAGCAACCTTGACAACG | 1350 |
| Qy | 1321 | GCATCTGCATCTGCTGCTCTCTGACAAAGAATPCTGCTGAGGAAGACTTTCGCAATCTG | 1380 |
| Db | 1321 | GCATCTGCATCTGCTCTCTCTGACAAAGAAATGCTGTGAGGAAGAGTCTTCGCAATCTG | 1380 |
| Qy | 1381 | AAGAGAGGAGAGAGGGGGCCGCAAGAACTTTTCCACTTCAAAAAAGCCAGAAGTCA | 1440 |
| Db | 1381 | AAGAGAGGAGAGAGGGGGCCGCAAGAACTTTTCCACTTCAAAAAAGCCAGAAGTCA | 1440 |
| Qy | 1441 | AAACGAGAGTGAATAAAGAAAGAACCCACAGAGGAGGAAGAAAGAAATGACCGAGAGAGGA | 1500 |
| Db | 1441 | AAACGAGAGTGAATAAAGAAAGAACCCACAGAGGAGGAAGAAAGAAATGACCGAGAGAGGA | 1500 |
| Qy | 1501 | AAACCAAGAGAGAGAGCCCAAGACCAAAAGGGGTCAAGAGAGAGGCCAAGTTGGCTTGAA | 1560 |
| Db | 1501 | AAACCAAGAGAGAGAGAGCCCAAGAGCCCAAAAGGGGTCAAGAGAGAGGCCAAGTTGGCTTGAA | 1560 |
| Qy | 1561 | TGGACCTCTCCAGCTGCGCTTCCCTGCTGAGTCCCTCAAGCTTTCTTTCCCC | 1611 |
| Db | 1561 | TGGACCTCTCCAGCTCTGGCTTCTCTGCTGAGTCCCTCAAGCTTTCTTTCCCC | 1611 |

| | | |
|----|--|---|
| | RESULT 2 | |
| | US-09-817-538-2 | |
| | / Sequence 2, Application US/098017538 | |
| | / Patent No. US20020137716ZAI | |
| | / GENERAL INFORMATION: | |
| | / APPLICANT: Li, Zuomei | |
| | / APPLICANT: Bonfils, Claire | |
| | / APPLICANT: Beesteman, Jeffrey | |
| | / TITLE OF INVENTION: Antisense oligonucleotide inhibition of Specific Histone | |
| | / TITLE OP INVENTION: Deacetylase Isoforms | |
| | / FILE REFERENCE: 106101.144 | |
| | / CURRENT APPLICATION NUMBER: US/09/817.538 | |
| | / PRIOR FILING DATE: 2001-03-26 | |
| | / PRIOR APPLICATION NUMBER: US 60/192,157 | |
| | / PRIOR FILING DATE: 2000-03-24 | |
| | / NUMBER OF SEQ ID NOS: 33 | |
| | / SOFTWARE: PatentIn version 3.1 | |
| | / SEQ ID NO 2 | |
| | / LENGTH: 1611 | |
| | / TYPE: DNA | |
| | / ORGANISM: Human | |
| | US-09-817-538-2 | |
| Qy | Query Match | 100.0%; Score 1610.6; DB 10; Length 1611; |
| | Best Local Similarity | 100.0%; Prid. No. 0; |
| | Matches 1611; Conservative | 0; Mismatches 0; Indels 0; Gaps 0; |
| Db | 1 ATGATCTGGGGGTCTCTGCGCCCGTGGTGCTGTCCTCCCATCGGTCAATCCTGAGAACACA | 60 |
| | | |
| | 1 ATGATCTGGGGGTCTCTGCCCGTGGTGCTGTCCTCCCATCGGTCAATCCTGAGAACACA | 60 |
| Qy | 61 GCCTGAGCGRCTCTGTCACTCGGGGTAGATCACGCGGGGAGGCGGACGAATGGCGCAGA | 120 |
| | | |
| | 61 GCCTGAGCGRCTCTGTCACTCGGGGTAGATCACGCGGGGAGGCGGACGAATGGCGCAGA | 120 |
| Db | 121 CGCAGGGCACC CGGAGGAAAGTCTGTTACTTACTA CTACGACGGGAGATTGGAAATTA CTAATT | 180 |
| | | |
| | 121 CGCAGGGCACC CGGAGGAAAGTCTGTTACTTA CTACGACGGGAGATTGGAAATTA CTAATT | 180 |
| Qy | 181 ATGACCAAGGCACCCCAATGAAAGCCTACCGCAATTCGCAATGACTCAATAATTGGTGCTCA | 240 |
| | | |
| | 181 ATGACCAAGGCACCCCAATGAAAGCCTACCGCAATTCGCAATGACTCAATAATTGGTGCTCA | 240 |
| Db | 241 ACTATGGTCTCTACCGAAAAATGGAATCTATGCGCCTCA CAAGCCAATGCTGAGAGAGA | 300 |
| | | |
| | 241 ACTATGGTCTCTACCGAAAAATGGAATCTATGCGCCTCA CAAGCCAATGCTGAGAGAGA | 300 |
| Qy | 301 TGACCAAGTACCAAGAGATGACTCAATTAATTCTTGCGCCTGCATCCGTCGAGATTAACA | 360 |
| | | |
| | 301 TGACCAAGTACCAAGAGATGACTCAATTAATTCTTGCGCCTGCATCCGTCGAGATTAACA | 360 |

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QY 361 TGTGGAGTACAGACAGATGACAGATTCAACCTTGATGAGACTGTCTGATATTG 420
DB 361 TGTGGAGTACAGACAGATGACAGATTCAACCTTGATGAGACTGTCTGATATTG 420
QY 421 ATGGCTGTGTTGAGTCTGTCACTGTCTGTCTGTCTGTCTGTCTGTCTGTCTG 480
DB 421 ATGGCTGTGTTGAGTCTGTCACTGTCTGTCTGTCTGTCTGTCTGTCTGTCTG 480
QY 481 TTAATAGAGAGAGAGAGAGATGCGCGTGAATTGGCTGGGGCTGACCAATGCAAGA 540
DB 481 TTAATAGAGAGAGAGAGAGATGCGCGTGAATTGGCTGGGGCTGACCAATGCAAGA 540
QY 541 AGTCCGAGGACATCTGCTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTG 600
DB 541 AGTCCGAGGACATCTGCTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTG 600
QY 601 TAAAGTATACCAAGAGAGAGAGAGATGATGATGATGATGATGATGATGATGATG 660
DB 601 TAAAGTATACCAAGAGAGAGAGAGATGATGATGATGATGATGATGATGATGATG 660
QY 661 AAGAGGCTTTTACACACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 720
DB 661 AAGAGGCTTTTACACACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 720
QY 721 ACTTCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 780
DB 721 ACTTCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 780
QY 781 TTAATACCTCCGCTCCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 840
DB 781 TTAATACCTCCGCTCCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 840
QY 841 TCAATGTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 900
DB 841 TCAATGTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 900
QY 901 ACTCCCTATCTGGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 960
DB 901 ACTCCCTATCTGGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 960
QY 961 GTGTGGAATTTGTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1020
DB 961 GTGTGGAATTTGTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1020
QY 1021 CCATTGTGAACGTGCGCGGTGCTGACATATGAGACAGCTGTGTGCTGTGATG 1080
DB 1021 CCATTGTGAACGTGCGCGGTGCTGACATATGAGACAGCTGTGTGCTGTGATG 1080
QY 1081 TCCCTATAGAGCTTCATATCAATGAGTACTTGAATATCTTGAACAGATTTCAAGCT 1140
DB 1081 TCCCTATAGAGCTTCATATCAATGAGTACTTGAATATCTTGAACAGATTTCAAGCT 1140
QY 1141 ACATCAGCTCTTCCATATATGATGATGATGATGATGATGATGATGATGATGATG 1200
DB 1141 ACATCAGCTCTTCCATATATGATGATGATGATGATGATGATGATGATGATGATG 1200
QY 1201 AGGAGCTGTTTGAAGACTTGAATGCTGCGACAGACTTGGGGTCTCAAAAGCAGCG 1260
DB 1201 AGGAGCTGTTTGAAGACTTGAATGCTGCGACAGACTTGGGGTCTCAAAAGCAGCG 1260
QY 1261 TTTCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1320
DB 1261 TTTCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1320
QY 1321 GCATCTGATCTGCTCTGACAAAGATGCTGTGTGAGAGAGATTTCCGATTTCTG 1380
DB 1321 GCATCTGATCTGCTCTGACAAAGATGCTGTGTGAGAGAGATTTCCGATTTCTG 1380
QY 1381 AAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1440
DB 1381 AAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1440
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QY 1441 AAACAGAGATGAAAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1500
DB 1441 AAACAGAGATGAAAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1500
QY 1501 AAACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1560
DB 1501 AAACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1560
QY 1561 TGAAGCTCTCCAGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1611
DB 1561 TGAAGCTCTCCAGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1611

RESULT 3
US-09-563-728A-25
; Sequence 25, Application US/09563728A
; Publication No. US20030078216A1
; GENERAL INFORMATION:
; APPLICANT: Macleod, Alan R
; APPLICANT: Li, Zoumei
; APPLICANT: Besterman, Jeffrey M
; TITLE OF INVENTION: Inhibition of Histone Deacetylase
; FILE REFERENCE: 106101.229
; CURRENT APPLICATION NUMBER: US/09/563,728A
; PRIOR FILING DATE: 2000-05-03
; PRIOR FILING DATE: 1999-05-03
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 25
; LENGTH: 1611
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-563-728A-25

Query Match 99.1%; Score 1596.6; DB 11; Length 1611;
Best Local Similarity 99.4%; Pred. No. 0;
Matches 1602; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 1 ATGTCTGGGGTCTCTGCGCGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 60
DB 1 ATGTCTGGGGTCTCTGCGCGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 60
QY 61 GCTGAGCGCTCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 120
DB 61 GCTGAGCGCTCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 120
QY 121 CGAAGGCAACCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 180
DB 121 CGAAGGCAACCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 180
QY 181 ATGAGCAAGGCAACCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 240
DB 181 ATGAGCAAGGCAACCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 240
QY 241 ACTATGCTCTTACCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 300
DB 241 ACTATGCTCTTACCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 300
QY 301 TGAAGATGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 360
DB 301 TGAAGATGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 360
QY 361 TGTGGAGTACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 420
DB 361 TGTGGAGTACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 420
QY 421 ATGGCTGTGTTGAGTCTGTCACTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTG 480
DB 421 ATGGCTGTGTTGAGTCTGTCACTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTG 480
QY 481 TTAATAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 540
DB 481 TTAATAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 540
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Db 643 TGTCTTTTCAATAGTAGAGAGATCTTCCAGGAACTGGGAGCTTACGGGATATCGGG 702
 Qy 757 CTGGCAAGAGCAAGATATATGCTGTTAACTACCCGCTCCGAGCGGGATTTGATGACAGT 816
 Db 703 CTGGCAAGAGCAAGATATATGCTGTTAACTACCCGCTCCGAGCGGGATTTGATGACAGT 762
 Qy 817 CCTATGAGCCATTTTCAAGCCGGCTATGCTCAAAATGAGATGTTCAAGCTTAGTG 876
 Db 763 CCTATGAGCCATTTTCAAGCCGGCTATGCTCAAAATGAGATGTTCAAGCTTAGTG 822
 Qy 877 CCGTGTCTTTACAGTGTGCTCAAGTCTCCATCTGCGGATCGGTTAGTGTCTTAATC 936
 Db 823 CCGTGTCTTTACAGTGTGCTCAAGTCTCCATCTGCGGATCGGTTAGTGTCTTAATC 882
 Qy 937 TATCTATCAAGAGACGCGCAAGTGTGGAATTTGTCAAGAGCTTTAACTGCGCATG 996
 Db 883 TATCTATCAAGAGACGCGCAAGTGTGGAATTTGTCAAGAGCTTTAACTGCGCATG 942
 Qy 997 TGTATGCTGGAGAGCGGTGTTACACCATTTCTTAACGTTGCCGGTCTGGACATATGAG 1056
 Db 943 TGTATGCTGGAGAGCGGTGTTACACCATTTCTTAACGTTGCCGGTCTGGACATATGAG 1002
 Qy 1057 CAGCTGTGCGCTGTGATACGAGATCCCTATATGAGCTTCCATATCAATGACTTTGAAT 1116
 Db 1003 CAGCTGTGCGCTGTGATACGAGATCCCTATATGAGCTTCCATATCAATGACTTTGAAT 1062
 Qy 1117 ACTTTGAGACCAAGTTTCAAGCTTCACATGATGCTTCCAAATATGACTTAACCAAGACGA 1176
 Db 1063 ACTTTGAGACCAAGTTTCAAGCTTCACATGATGCTTCCAAATATGACTTAACCAAGACGA 1122
 Qy 1177 ATGAGTACCTGAGAGATCAAAACAGCGACTGTTTGAAGACCTTAGAATGCTGCCAGC 1236
 Db 1123 ATGAGTACCTGAGAGATCAAAACAGCGACTGTTTGAAGACCTTAGAATGCTGCCAGC 1182
 Qy 1237 CACTTGGGGTCCAACCGCAGCGATTCTTGAGAGCGCCATCCCTGAGAGAGTGGCGATG 1296
 Db 1183 CACTTGGGGTCCAACCGCAGCGATTCTTGAGAGCGCCATCCCTGAGAGAGTGGCGATG 1242
 Qy 1297 AGAGACGAAGACGACCTGACAGAGCGATCTGCATCTGCTCTTGACAAACGAATGGCT 1356
 Db 1243 AGAGACGAAGACGACCTGACAGAGCGATCTGCATCTGCTCTTGACAAACGAATGGCT 1302
 Qy 1357 GTGAGGAAGAGTCTCCGATTCTGAAGAGAGGAGGAGGCGGCGCAAGACCTTTCCA 1416
 Db 1303 GTGAGGAAGAGTCTCCGATTCTGAAGAGAGGAGGAGGCGGCGCAAGACCTTTCCA 1362
 Qy 1417 ACTTCAAAAAAGCCAAAGAGATCAAAACAGAGATGAAAAAGAAAAGACCCAGAGAGA 1476
 Db 1363 ACTTCAAAAAAGCCAAAGAGATCAAAACAGAGATGAAAAAGAAAAGACCCAGAGAGA 1422
 Qy 1477 AGAAAGGAATCAACCGAAGAGAGAGAAAAACAAAGAGAGAAACCAAGAGGAGGTCA 1536
 Db 1423 AGAAAGGAATCAACCGAAGAGAGAGAAAAACAAAGAGAGAAACCAAGAGGAGGTCA 1482
 Qy 1537 AGAGAGAGGCAAGTGGCTGATGAGACTCTCCAGCTCTGGCTTCTGCTGAGTCCCT 1596
 Db 1483 AGAGAGAGGCAAGTGGCTGATGAGACTCTCCAGCTCTGGCTTCTGCTGAGTCCCT 1542
 Qy 1597 CACGTTTCTTTCCC 1610
 Db 1543 CACGTTTCTTTCCC 1556

RESULT 5
 US-09-925-300-623
 ; Sequence 623, Application US/09925300
 ; Patent No. US20020151681A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Craig Kosen,
 ; APPLICANT: Steve Ruben
 ; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
 ; FILE REFERENCE: PA101
 ; CURRENT APPLICATION NUMBER: US/09/925,300

; CURRENT FILING DATE: 2001-08-10
 ; PRIOR APPLICATION NUMBER: PCT/US00/05988
 ; PRIOR FILING DATE: 2000-03-08
 ; PRIOR APPLICATION NUMBER: 60/124,270
 ; PRIOR FILING DATE: 1999-03-12
 ; NUMBER OF SEQ ID NOS: 1890
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 623
 ; LENGTH: 2163
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: misc feature
 ; LOCATION: (29)
 ; OTHER INFORMATION: n equals a,t,g, or c
 US-09-925-300-623

Query Match 93.1%; Score 1499.6; DB 10; Length 2163;

Best Local Similarity 99.4%; Pred. No. 0; Matches 1505; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

Qy 97 GGGAGGCGGCAAGATGGCGCAGACGCGACCGCGGAGAAAGTCTGTACTACTAG 156
 Db 71 GGGAGGCGGCAAGATGGCGCAGACGCGACCGCGGAGAAAGTCTGTACTACTAG 130
 Qy 157 ACGGGGATGTTGGAATTAATTAATGACAAAGGCCAATGAAAGCTTCAACCGAATCC 216
 Db 131 ACGGGGATGTTGGAATTAATTAATGACAAAGGCCAATGAAAGCTTCAACCGAATCC 190
 Qy 217 GCATGACTATTAATTTGCTGCTCAACTATGTTCTCTACCGAATAATGAAATCTATCGCC 276
 Db 191 GCATGACTATTAATTTGCTGCTCAACTATGTTCTCTACCGAATAATGAAATCTATCGCC 250
 Qy 277 CTCAGAAAGCCAAATGCTGAGAGATGACCAAGTACCAAGCGATGACTATTAATTC 336
 Db 251 CTCAGAAAGCCAAATGCTGAGAGATGACCAAGTACCAAGCGATGACTATTAATTC 310
 Qy 337 TGGGCTCCATCCGTCAGATTAATGATGAGTACAGAGAGATGACAGATTTCAAG 396
 Db 311 TGGGCTCCATCCGTCAGATTAATGATGAGTACAGAGAGATGACAGATTTCAAG 370
 Qy 397 TTGTGAGAGACTGTCAGATTTGATGAGGCTGTTGAGTCTGTCAAGTTTCTACTGTG 456
 Db 371 TTGTGAGAGACTGTCAGATTTGATGAGGCTGTTGAGTCTGTCAAGTTTCTACTGTG 430
 Qy 457 GTTCTGTGCAAGTGTGGAATTAATTAACAGAGAGCAATCGCGTGAATTTGG 516
 Db 431 GTTCTGTGCAAGTGTGGAATTAATTAACAGAGAGCAATCGCGTGAATTTGG 490
 Qy 517 CTGGGGGCTGCAACATGCAAGAAAGTCCGAGGATCTGGCTTCTGTAAGTATGATA 576
 Db 491 CTGGGGGCTGCAACATGCAAGAAAGTCCGAGGATCTGGCTTCTGTAAGTATGATA 550
 Qy 577 TCGTCTTTGCACTCTGGAATCTGTAAGTATCAACAGAGGCTGTAACATTTGACATTG 636
 Db 551 TCGTCTTTGCACTCTGGAATCTGTAAGTATCAACAGAGGCTGTAACATTTGACATTG 610
 Qy 637 ATATTACCATGATGACGCGGTGGAAGAGAGCTTTCAACACCGGACCGGCTATGAC 696
 Db 611 ATATTACCATGATGACGCGGTGGAAGAGAGCTTTCAACACCGGCTATGAC 670
 Qy 697 TGTCTTTTCAATAGTAGAGAGTCTTCCAGGAAGTGGGAGCTTACCGGATATCGGG 756
 Db 671 TGTCTTTTCAATAGTAGAGAGTCTTCCAGGAAGTGGGAGCTTACCGGATATCGGG 730
 Qy 757 CTGGCAAGAGCAAGATTAATGCTGTTAACTACCCGCTCCGAGCGGATTTGATGACGAGT 816
 Db 731 CTGGCAAGAGCAAGATTAATGCTGTTAACTACCCGCTCCGAGCGGATTTGATGACGAGT 790
 Qy 817 CCTATGAGCCATTTTCAAGCCGGCTATGCTCAAAATGAGATGTTCCAGGCTTAGTG 876
 Db 791 CCTATGAGCCATTTTCAAGCCGGCTATGCTCAAAATGAGATGTTCCAGGCTTAGTG 850

877 CGGTGCTCTTACAGTGTGCTCAGACTCCCTATCTGGGAGTCCGTAGTGTCTTCAATC 936
851 CGGTGCTCTTACAGTGTGCTCAGACTCCCTATCTGGGAGTCCGTAGTGTCTTCAATC 910
937 TATCTATCAAGAGACAGCCCAAGTGTGTGAATTTGTCAAGAGCTTTAACTGCTTATGC 996
911 TAACTATCAAGAGACAGCCCAAGTGTGTGAATTTGTCAAGAGCTTTAACTGCTTATGC 970
997 TGAAGCTGGGAGGGGGGGTGTGTACACACTGTGTAAAGTTGGCCGGTGGGACATATAGA 1056
971 TGAAGCTGGGAGGGGGGGTGTGTACACACTGTGTAAAGTTGGCCGGTGGGACATATAGA 1030
1057 CAGCTGTGGCCCTGATATCGAGAGATCCCTATATGAGCTTCCATACATATGACTACTTGAAT 1116
1031 CAGCTGTGGCCCTGATATCGAGAGATCCCTATATGAGCTTCCATACATATGACTACTTGAAT 1090
1117 ACTTTGAGCCAGATTTCAAGTCCATCATCATGCTCTTCCATATATATATATATATATATAT 1176
1091 ACTTTGAGCCAGATTTCAAGTCCATCATCATGCTCTTCCATATATATATATATATATATAT 1150
1177 ATGAGTACCTGGAGAGATGCAACAGAGAGCTGTTTGAAGACCTTAGATGCTGCGGACG 1236
1151 ATGAGTACCTGGAGAGATGCAACAGAGAGCTGTTTGAAGACCTTAGATGCTGCGGACG 1210
1237 CACCTGGGGTCCAAACGAGGCGAGATTCCTGAGAGAGCCCATCCCTGAGAGAGTGGCGATG 1296
1211 CACCTGGGGTCCAAACGAGGCGAGATTCCTGAGAGAGCCCATCCCTGAGAGAGTGGCGATG 1270
1297 AGAGCAAGAGAGAGCTGTGACAAAGCGCATCTGATCTGCTCTTGAACAAAGAAATGGCT 1356
1271 AGAGCAAGAGAGAGCTGTGACAAAGCGCATCTGATCTGCTCTTGAACAAAGAAATGGCT 1330
1357 GTGAGAGAGAGTCTTCCGATCTTGAAGAGAGAGAGAGGGGGGCGGAAAGACTCTTCCA 1416
1331 GTGAGAGAGAGTCTTCCGATCTTGAAGAGAGAGAGAGGGGGGCGGAAAGACTCTTCCA 1390
1417 ACTTCAAAAAAGCCAAAGAGAGTCAAAAAGAGAGTGAAGAGAGAGAGAGAGAGAGAGAGAG 1476
1391 ACTTCAAAAAAGCCAAAGAGAGTCAAAAAGAGAGTGAAGAGAGAGAGAGAGAGAGAGAGAG 1450
1451 AGAAGAGAGAGTCAAG 1510
1337 AGAGAGAGAGAGTGTGGCTGATGAGCTCTCAGCTGCTGCTTCTGCTGAGTGGCT 1596
1511 AGAGAGAGAGTCAAGTGTGGCTGATGAGCTCTCAGCTGCTGCTTCTGCTGAGTGGCT 1570
1597 CACGTTTCTTCCC 1610
1571 CACGTTTCTTCCC 1584

RESULT 6
US-09-754-167-3
Sequence 3, Application US/09754167
Patent No. US20010019328A1
GENERAL INFORMATION:
APPLICANT: Brect P. Monia
APPLICANT: Jacqueline Wyatc
TITLE OF INVENTION: ANTISENSE MODULATION OF HISTONE DEACETYLASE 1 EXPRESSION
FILE REFERENCE: RUS-0140
CURRENT APPLICATION NUMBER: US/09/754.167
CURRENT FILING DATE: 2000-12-19
NUMBER OF SEQ ID NOS: 87
SEQ ID NO 3
LENGTH: 2091
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (64) ... (1512)
US-09-754-167-3

Query Match 93.0%; Score 1498; DB 9; Length 2091;
Best Local Similarity 99.3%; Pred. No. 0;
Matches 1504; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

97 GGGAGGCGAGCAAGATGCGCCAGACCGAGGCGACCCGGAGAGAAAGTGTACTACTACG 156
50 GGGAGGCGAGCAAGATGCGCCAGACCGAGGCGACCCGGAGAGAAAGTGTACTACTACG 109
157 ACGGGAGTGTGAATTTACTATTATGAGCAAGAGCCACCCCAATGAAGCCACCGAATCC 216
110 ACGGGAGTGTGAATTTACTATTATGAGCAAGAGCCACCCCAATGAAGCCACCGAATCC 169
217 GCATGACTCATATTTGCTGCTCACTATGCTCTTACCGAAAAATGAAATCTATCGCC 276
170 GCATGACTCATATTTGCTGCTCACTATGCTCTTACCGAAAAATGAAATCTATCGCC 229
277 CTCACAAAGCCAAATGCTGAGAGATGACCAAGTACACAGCGATGACTATTAATTTCT 336
230 CTCACAAAGCCAAATGCTGAGAGATGACCAAGTACACAGCGATGACTATTAATTTCT 289
337 TGGGCTCCATCGGTCCAGATPACATGTCGAGATGACCAAGAGATGACAGATTCACG 396
290 TGGGCTCCATCGGTCCAGATPACATGTCGAGATGACCAAGAGATGACAGATTCACG 349
397 TTGGTGAAGACTGTCCAGATTTGATGAGCTGTTTGAAGTCTGTCAAGTGTCTACTGCTG 456
350 TTGGTGAAGACTGTCCAGATTTGATGAGCTGTTTGAAGTCTGTCAAGTGTCTACTGCTG 409
457 GTTCTGTGGCAAGTGTGTGAACTTATATAGACAGACAGACGATCCCGTGAATTTGG 516
410 GTTCTGTGGCAAGTGTGTGAACTTATATAGACAGACAGACGATCCCGTGAATTTGG 469
517 CTGGGGGCTTGCACATGCAAGAGTCCGAGCATCTGGCTCTGTAGTCAATGATA 576
470 CTGGGGGCTTGCACATGCAAGAGTCCGAGCATCTGGCTCTGTAGTCAATGATA 529
577 TCGCTTGGCCATCTCTGAGAACTGTAAAGTATCACACAGAGGAGTGTACTTGAATTG 636
530 TCGCTTGGCCATCTCTGAGAACTGTAAAGTATCACACAGAGGAGTGTACTTGAATTG 589
637 ATATTCACATGTGTGAGCGGCTGAGAGAGGCTTTTACACACAGAGCGGCTCATGACTG 696
590 ATATTCACATGTGTGAGCGGCTGAGAGAGGCTTTTACACACAGAGCGGCTCATGACTG 649
697 TGTCTTTTCAATGATGAGAGTACTTCCAGAGAACTGGGGACCTACCGGATACCGGGG 756
650 TGTCTTTTCAATGATGAGAGTACTTCCAGAGAACTGGGGACCTACCGGATACCGGGG 709
757 CTGGCAAGACAGATTTATGCTGTTTAACTACCCGCTCCGAGACGGGATGATGACGAGT 816
710 CTGGCAAGACAGATTTATGCTGTTTAACTACCCGCTCCGAGACGGGATGATGACGAGT 769
817 CTTATGAGGCCATTTTCAAGCCGCTCATGTCACAAAGTATGAGAGTTCACGCTTATG 876
770 CTTATGAGGCCATTTTCAAGCCGCTCATGTCACAAAGTATGAGAGTTCACGCTTATG 829
877 CGGTGCTCTTACAGTGTGCTCAGACTCCCTATCTGGGAGTCCGTTAAGTGTCTTCAATC 936
830 CGGTGCTCTTACAGTGTGCTCAGACTCCCTATCTGGGAGTCCGTTAAGTGTCTTCAATC 889
937 TATCTATCAAGAGACAGCCCAAGTGTGTGAATTTGTCAAGAGCTTTAACTGCTTATGC 996
890 TAACTATCAAGAGACAGCCCAAGTGTGTGAATTTGTCAAGAGCTTTAACTGCTTATGC 949
997 TGAAGCTGGGAGGGGGGGTGTGTACACACTGTGTAAAGTTGGCCGGTGGGACATATAGA 1056
950 TGAAGCTGGGAGGGGGGGTGTGTACACACTGTGTAAAGTTGGCCGGTGGGACATATAGA 1009
1057 CAGCTGTGGCCCTGATATCGAGAGATCCCTATATGAGCTTCCATACATATGACTACTTGAAT 1116
1010 CAGCTGTGGCCCTGATATCGAGAGATCCCTATATGAGCTTCCATACATATGACTACTTGAAT 1069

QY 1117 ACTTGGACCAATTTCAGCTCCATCATCTCTTCCATATGACTTAACAGACGCA 1176
DB 1070 ACTTGGACCAATTTCAGCTCCATCATCTCTTCCATATGACTTAACAGACGCA 1129
QY 1177 ATGAGTACCTCGAGAGATCAACAGGACTGTTTGAACCTTAGATCTCCGACG 1236
DB 1130 ATGAGTACCTCGAGAGATCAACAGGACTGTTTGAACCTTAGATCTCCGACG 1189
QY 1237 CACCTGGGGTCAAAAGCAGGCGATCTGAGAGCGCATCCCTGAGGAGAGGCGATG 1296
DB 1190 CACCTGGGGTCAAAAGCAGGCGATCTGAGAGCGCATCCCTGAGGAGAGGCGATG 1249
QY 1297 AGGACGAGAGCAGCCTGACAGGCGATCTGATCTGCTCTGCAAAAGATTGCTT 1356
DB 1250 AGGACGAGAGCAGCCTGACAGGCGATCTGATCTGCTCTGCAAAAGATTGCTT 1309
QY 1357 GTGAGAGAGGTTCTCCGATCTGAGAGAGGAGGAGGCGCGCAGAGACTTTCCA 1416
DB 1310 GTGAGAGAGGTTCTCCGATCTGAGAGAGGAGGAGGCGCGCAGAGACTTTCCA 1369
QY 1417 ACTTCAAAAAAGCAGAGAGTCAAAACAGAGATGAAAAGAAAAGCCAGAGGAGA 1476
DB 1370 ACTTCAAAAAAGCAGAGAGTCAAAACAGAGATGAAAAGAAAAGCCAGAGGAGA 1429
QY 1477 AGAAGGAATCAACGAGAGAGAGAAAACAAAGAGAGAGAGCCAGAGCGGCTCA 1536
DB 1430 AGAAGGAATCAACGAGAGAGAGAGAAAACAAAGAGAGAGAGCCAGAGCGGCTCA 1489
QY 1537 AGAGAGAGCCAGAGTGGCTGAGATGAGCTTCTCAGCTCTGCTCTGCTGATCCT 1596
DB 1490 AGAGAGAGCTCAAGTGGCTGAGATGAGCTTCTCAGCTCTGCTCTGCTGATCCT 1549
QY 1597 CAGCTTCTTTCC 1610
DB 1550 CACGTTCTTCC 1563

RESULT 7

US-09-563-728A-27
; Sequence 27, Application US/09563728A
; Publication No. US2003078216A1
; GENERAL INFORMATION:
; APPLICANT: Macleod, Alan R
; APPLICANT: Li, Zoumei
; APPLICANT: Besteman, Jeffrey M
; TITLE OF INVENTION: Inhibition of Histone Deacetylase
; FILE REFERENCES: 106101.229
; CURRENT APPLICATION NUMBER: US/09/563.728A
; PRIOR FILING DATE: 2000-05-03
; PRIOR FILING DATE: 1998-05-03
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: Patencin Ver. 2.1
; SEQ ID NO 27
; LENGTH: 1985
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-563-728A-27

Query Match 50.0%; Score 805.2; DB 11; Length 1985;
Best Local Similarity 72.8%; Pred. No. 3.1e-237;
Matches 1088; Conservative 0; Mismatches 388; Indels 0; Gaps 0;

QY 126 GGCACCCGAGAGAGTCTTACTACTACGACGGGAGTTGGAAATTACTATATGA 185
DB 223 GGCAGGCAAAAAAGTCTCTCTACTACTACGACGGGATATGGAATATTTATATGA 282
QY 186 CAGGACCACTCAAGAGCTCAACGAGATGAGTCAATTAATTGCTGCTCACTAT 245
DB 283 CAGGATCATCTCAAGAGCTCAATGAGATGAGTCAATTAATTGCTGCTCACTAT 342
QY 246 GGTCTTACGAGAAATGAAATCTATGCTTCAAAAGCAATGCTGAGAGATGACC 305
DB 1423 TCTATTCAGATCAGACAAAGGAGATGCTTGTGATGAAGATTTCTAGATTCAGAT 1482

DB 343 GGTATATACAAAAATGAAATATATAGCCCCCATTAAGCACTGCCCCAAGAAATGACA 402
QY 306 AAGTACCAAGAGATGATCAATTAATCTTGGCGCTCATCCGTCCAGATTAACATGTG 365
DB 403 AATATACAGAGATGATGATATCAATTTCTACGGTCAATTAAGCAAGATTAACATGTCT 462
QY 366 GAGTACAGAGAGATGAGATTAATCAAGTTGGAGGAGACTGTCCAGTATTCATGTGC 425
DB 463 GAGTATAGTACAGATGATATATTAATGTTGAGAAAGATTTGTCCACGTTTATGGA 522
QY 426 CTGTTGAGTCTGTCAAGTTGCTACTGAGTGTCTGTGAGCAAGTCTGTGAATTTAAT 485
DB 523 CTGTTGAGTCTGTCAAGTTGCTACTGAGTGTCTGTGAGCAAGTCTGTGAATTTAAT 582
QY 486 AAGCAGACAGAGATGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGT 545
DB 583 CAGACAGACAGATGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAG 642
QY 546 GAGGATCTGCTCTGTTACGTCATGATATCTGTTGGCCTCTGGAACCTGTAAG 605
DB 643 GAGGATCTGAGATCTGTTACGTTATGATATTTGTCTGCAATCTTGAATTAATTAAG 702
QY 606 TATCACCAGAGGCTGTATCAATGATGATTAATCAATGATGAGCGGCTGAGAG 665
DB 703 TATCATCAGAGATCTTATATATGATATGATATTAATCAATGATGATGATGATGATG 762
QY 666 GCTTCTTACACGAGACCGGCTCAATGATGATGATGATGATGATGATGATGATGATG 725
DB 763 GCTTCTTATCAACAGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 822
QY 726 CCAGAACTGGGAGCTTACGAGGATACCGGAGTACCGGAGAAAGCAAGTATGCTGTTAAC 785
DB 823 CTTGAGCAGAGAGATCTTGGAGATTTGCTGCTGAGAAAGCAATATCTATGCTGCAAT 882
QY 786 TACCGCTCCAGACGAGATGATGATGATGATGATGATGATGATGATGATGATGATG 845
DB 883 TTTCCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 942
QY 846 TCCAAAGTATGAGATGTTCCAGCTATGCTGAGTGTGCTTACAGTGTGCTCAAGCTCC 905
DB 943 TCAAGGATGATGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1002
QY 906 CTATCTGGGAGATCGTTAGTGTGCTTCAATCTATCATCAAAAGACAGCGCAAGTGTG 965
DB 1003 TATCTGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1062
QY 966 GAATTTGCAAGAGCTTTAATCTGCTATGATGATGATGATGATGATGATGATGATGAT 1025
DB 1063 GAAATGTAAGAACTTTAATCTGCTATGATGATGATGATGATGATGATGATGATGAT 1122
QY 1026 CTTAAGCTTGGCGGTGCTGAGATGATGATGATGATGATGATGATGATGATGATGAT 1085
DB 1123 CTTAAGCTTGGCGGTGCTGAGATGATGATGATGATGATGATGATGATGATGATGAT 1182
QY 1086 AATGAGCTTCAATTAAGTACTTGAATCTTGAATCTTGAATCTTGAATCTTGAATCTT 1145
DB 1183 AATGAGCTTCAATTAAGTACTTGAATCTTGAATCTTGAATCTTGAATCTTGAATCTT 1242
QY 1146 AGTCTTCCAAATATGATCAATCAAGAAAGATGATGATGATGATGATGATGATGATG 1205
DB 1243 AGTCTTCCAAATATGATCAATCAAGAAAGTCAATGATGATGATGATGATGATGATG 1302
QY 1206 CTGTTGAGAACTTGAATGCTGCGGACGCACTGCGGAGTCCAAAGCGAGATTTCT 1265
DB 1303 TTTGTTGAAATTTGCGATGTTACTCTCAATGACCTGAGTGTCAAGATGATTTCCA 1362
QY 1266 GAGGAGCAGATCCGAGAGAGAGTGGCGATGAGAGAGAGAGAGAGAGAGAGAGAG 1325
DB 1363 GAGGAGCTGCTTCAAG 1422
QY 1326 TCGATCTGCTCTGACAAAGAAATGCTGTGAGAGAGAGAGAGAGAGAGAGAGAGAG 1385
DB 1423 TCTATTCAGATCAGACAAAGGAGATGCTTGTGATGAAGATTTCTAGATTCAGAT 1482

QY 1386 GAGGAGAGGGGGCCGCAAGACTCTTCAACTTCAAAAAAGCAGAGTCAAAACA 1445
Db 1483 GAAGAGAGAGAGGTCCAGAAAATGTGGCTGATCATTAAGAAAGACAAAGAAAGCTAAGA 1542
QY 1446 GAGGATGAAAAAGAAAAGACCAGAGAGAGAAAGAAAGAAATCACCGAAGAGAGAAACC 1505
Db 1543 ATTGAAGAGATTAAGAAAGAAACAGAGAGCAAAAAACAGCGTTAAGAAAGATTA 1602
QY 1506 AAGGAGAGAAAGCAAGAACCAAGGGGTCAAGAGAGGCGCAAGT 1551
Db 1603 TCCAAGGACAAAGTGTGAAAAAACAAGATACCAAGAGAACCAAT 1648

RESULT 8
US-09-373-658-76
; Sequence 76, Application US/09373658
; Publication No. US20030092900A1
; GENERAL INFORMATION:
; APPLICANT: Irueña-Arlepe, Luisa
; APPLICANT: Haselings, Gregg A.
; APPLICANT: Ruben, Steven W.
; APPLICANT: Jonak, Zdenka L.
; APPLICANT: Trull, Stephen H.
; APPLICANT: Fromwald, James A.
; APPLICANT: Terrett, Jonathan A.
; TITLE OF INVENTION: Meth1 and Meth2 polynucleotides and polypeptides
; FILE REFERENCE: 1488.1070006
; CURRENT APPLICATION NUMBER: US/09/373.658
; NUMBER OF FILING DATE: 1999-08-13
; NUMBER OF SEQ ID NOS: 125
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 76
; LENGTH: 1985
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: Unknown
US-09-373-658-76

Query Match 50.0%; Score 805.2; DB 11; Length 1985;
Best Local Similarity 72.8%; Pred. No. 3.1e-237;
Matches 1038; Conservative 0; Mismatches 388; Indels 0; Gaps 0;

QY 126 GGCACCCGAGAGAAAGTCTGTACTACTACAGACCGGGATGTTGGAAAAATTAATTAAGA 185
Db 223 GCGCGCAAAAAAAGTCTGTACTACTACAGACCGGTATTTGAAAAATTAATTAAGA 282
QY 186 CAAGGCAACCAATGAAGCTCACCGAATCCGATGATCACTAAATTTGCTGCTCAACTAT 245
Db 283 CAGGCTATCCCATGAGCTCATAGAAATCCGATGATCACTAAATTTGCTGCTCAACTAT 342
QY 246 GGTCTTACCGAAAAATGAATCTATGCGCTCACAAAAGCAATGCTGAGAGATGAC 305
Db 343 GCGTTATACAAAAAATGAATATATAGGCCCTTAAGCCACATGCGAAAGATGACA 402
QY 306 AAGTACCAACAGATGATTAATTAATTTGCGCTCATCCGTCGATTAAGATGCG 365
Db 403 AAATATCAAGTATGATATATATCAATTTCTACGCTCAATTAAGCCAGATTAACATGCT 462
QY 366 GAGTACAGCAAGATGATCAAGATTCACCTGGTGAAGACTGTCAGATTTGATGAGC 425
Db 463 GAGTATAGTAAAGATGATCAATTAATTTGAGAGAAATGTCGACGCTTTGATGGA 522
QY 426 CTGTTGAGTTCTGCTGATGCTTACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 485
Db 523 CTCTTGTGTTTGTGCACTCTCAACTGCGCTTCAAGTCTGAGAGCTGTAAGTAAAC 582
QY 486 AAGGAGAGAGAGATGATGAGATTTGAGATTTGAGATTTGAGATTTGAGATTTGAG 545
Db 583 CGAAGAGAGAGATGATGAGATTTGAGATTTGAGATTTGAGATTTGAGATTTGAGAT 642
QY 546 GAGGATCTGGCTTCTGTTAGCTCAATATGCTTGGCGATCTGGAATCTGTAAG 605

Db 643 GAAGCATCAGAGATTCGTGTTAGTTAATGATATGTGCTTCCATCTCTTAATTAAG 702
QY 606 TATCACAAGAGGTGCTGATCATTTGATTAATTTCAACATGATGACCGCGTGAAGAG 665
Db 703 TATCATCAGAGATCTTATATATGATTAATTAATTAATTAATTAATTAATTAATTA 762
QY 666 GCTTCTACACCAAGGACCGGCTCATGACTGTGCTCTTCAATTAATTAATTAATTA 725
Db 763 GCTTTTATTAACAAGATGCTGATTAATGACGCTATCATTTCAATTAATTAATTA 822
QY 726 CAGAACTGGGAGCTTACCGGATTAACCGGCTGGCAAGAAAGATTAATGCTTTAAC 785
Db 823 CTGGGACAGAGACTTGAAGGATTAATGCTGTAAGAAAGCAAAATTAATTAATTA 882
QY 786 TACCGCTCGAAGCGGATTTGATGACGATCCTTAAGAGCCATTTCAAGCGGCTATG 845
Db 883 TTTCCAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 942
QY 846 TCCAAGATTAAGAGATGTTCCAGCTAGTGGCGGTCTTACAGTGTGCTCAGACTCC 905
Db 943 TCAGAGTATGAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1002
QY 906 CTATCTGGGATGCTTGAAGTGTGCTTCAATCTATCTATCAAGGACACGCAAGTGTG 965
Db 1003 TTAATCTGATAGACTGGGTGTTCAATCTAACAGTCAAGGTCATGCTTAATGTGA 1062
QY 966 GAATTTGTCAAGCTTTTAACTGCTGATGATGATGATGATGATGATGATGATGAT 1025
Db 1063 GAAGTGTAAACCTTTTAACTTCACTATGATGATGATGATGATGATGATGATGAT 1122
QY 1026 CGTAACTGCGGCTGCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 1085
Db 1123 CGTAACTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1182
QY 1086 AATGAGCTTCATTAAGATGATGATGATGATGATGATGATGATGATGATGATGAT 1145
Db 1183 AATGAGTTCATTAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1242
QY 1146 AGTCTTCCAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1205
Db 1243 AGTCTTCCAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1302
QY 1206 CTGTTTGAAGCTTGAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1265
Db 1303 TTGTTTGAAGCTTGAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1362
QY 1266 GAGGACGCTATCCCTGAGAGATGATGATGATGATGATGATGATGATGATGATGAT 1325
Db 1363 GAAGATGCTGTTATGAGAGATGATGATGATGATGATGATGATGATGATGATGATGAT 1422
QY 1326 TCGATGCTGCTCTGACAAAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1385
Db 1423 TCTATTCGACATCAAGCAAGGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1482
QY 1386 GAGGAGAGGGGGCCGCAAGAACTCTTCAACTTCAAAAAAGCAGAGATCAAAACA 1445
Db 1483 GAAGAGAGAGAGTCCAGAAAATGTGGCTGATCATTAAGAAAGACAAAGAAAGCTAAGA 1542
QY 1446 GAGGATGAAAAAGAAAAGACCAGAGAGAGAAAGAAAGAAATCACCGAAGAGAGAAACC 1505
Db 1543 ATTGAAGAGATTAAGAAAGAAACAGAGAGCAAAAAACAGCGTTAAGAAAGATTA 1602
QY 1506 AAGGAGAGAAAGCAAGAACCAAGGGGTCAAGAGAGGCGCAAGT 1551
Db 1603 TCCAAGGACAAAGTGTGAAAAAACAAGATACCAAGAGAACCAAT 1648

RESULT 9
US-10-177-293-205
; Sequence 205, Application US/10177293
; Publication No. US20030124128A1
; GENERAL INFORMATION:

APPLICANT: Lillie, James
APPLICANT: Galt, Karen
APPLICANT: Zhao, Xumei
APPLICANT: Kamnavorpu, Manjula
APPLICANT: Kamnavor, Shubhangi
APPLICANT: Mertens, Maureen
APPLICANT: Myer, Vic
APPLICANT: Wang, Youzhen
APPLICANT: Xu, Yongyao
APPLICANT: Hoersch, Sebastian
APPLICANT: Monahan, John
APPLICANT: Meyers, Rachel E.
APPLICANT: Bast Jr., Robert C.
APPLICANT: Hortobagyi, Gabriel N.
APPLICANT: Puzsrai, Lajos
APPLICANT: Meric, Punda
APPLICANT: Sahin, Aysegul
APPLICANT: Mills, Gordon B.
TITLE OF INVENTION: COMPOSITIONS, KITS, AND METHODS FOR IDENTIFICATION, ASSESSMENT,
FILE REFERENCE: PREVENTION, AND THERAPY OF BREAST CANCER
FILE REFERENCE: MRI-038
CURRENT APPLICATION NUMBER: US/10/177,293
CURRENT FILING DATE: 2002-06-21
PRIOR APPLICATION NUMBER: US 60/299,887
PRIOR FILING DATE: 2001-06-21
PRIOR APPLICATION NUMBER: US 60/301,572
PRIOR FILING DATE: 2001-06-27
PRIOR APPLICATION NUMBER: US 60/306,501
PRIOR FILING DATE: 2001-07-18
PRIOR APPLICATION NUMBER: US 60/325,002
PRIOR FILING DATE: 2001-09-25
PRIOR APPLICATION NUMBER: US 60/362,585
PRIOR FILING DATE: 2002-03-05
PRIOR APPLICATION NUMBER: US 60/xxx,xxx
PRIOR FILING DATE: 2002-05-14
NUMBER OF SEQ ID NOS: 506
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 205
LENGTH: 1985
TYPE: DNA
ORGANISM: Homo sapiens
US-10-177-293-205

Query Match 50.0%; Score 805.2; DB 14; Length 1985;
Best Local Similarity 72.8%; Pred. No. 3.1e-237;
Matches 1038; Conservative 0; Mismatches 388; Indels 0; Gaps 0;

126 GGACACCGAGGAAAGTCTGTTACTACTACGACGGGAGATGTTGAAATTACTATTATGGA 185
223 GGCGGAGAAAAAATCTGCTACTACTACGACGGGATATTTGAAATTATTTATGGA 282
186 CAAGGCCACCAATGAAAGCTCTACCGAATCCGATATCTATATTTGCTGCTCAACTAT 245
283 CAGGGTCATCTCCATGAAGCTCTCATAGATCCGATGACCCATTAATTGCTGTTAAATTAT 342
246 GGTCTTACCGAATAATGAAATCTATCGCCCTCAAAAGCCAAATGCTGAGAGAAC 305
343 GGTTCATACGAAAAATGAAATATATAGGCCCATTAAGCCATGCGGAGAAATGACA 402
306 AAGTACCAAGCATGATCTATTAATTTCTGCGCTCCATCCGTCAGATACATGTCG 365
403 AATATACAGATGATGATATCAATTTCTACGGCTCAATAGACCAATACATATCTCT 462
366 GAGTACAGCAAGATGACAGATTCACGTTGGTGAAGACTGTCAGTATTCGATGCG 425
463 GAGTATAGTAAAGATGATCATATATTTAATGTTGAGAAATGTCACAGGCTTGAATGA 522
426 CTGTTGAGTCTGCTAGTCTCTACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 485
523 CTCTTGAAGTTTGTGCTGCTCTCAACTGCGGCTTCAAGTCTGAGTGTGAAGTTAAC 582
486 AAGCAGCAGACGACATCGCGTGAATTGGGCTGCGGCGCTGACCATGCAAGAAAGTCC 545

583 CGACAAACAGATGATATGCTGTTAATTTGGCTGAGCATTTACATCATCTTAAGAAATAC 642
546 GAGGATCTGCTGCTGTTTACGTCATGATATGTTGGCATCTGGAACCTGCTAAAG 605
643 GAGCATGAGATTTCTGTTACTTAATGATATTTGTCCTGCAATCTTGAATTTACTAAAG 702
606 TATCAACCAAGAGGTGCTGATCAATTGACATTTATTTACCATGATGACCGCTGGAAG 665
703 TATCATGAGAGATCTTATATATTTATATGATATTTATCATCATGATGATGTTGAAGAA 762
666 GCTTCTACACCAAGGACCGGCTCATGCTGCTGCTTCTGATATGATGAGATGCTTC 725
763 GCTTTTATACAAAGATCTGTTATATGAGATATTTCAATTAATTTGAGATCTTT 822
726 CCAGGAATCGGGGACCTTACCGGATACCGGGCTGCAAGACAAAGATATGCTGTTAAC 785
823 CTTGGCACAGACATTTGAGGATATTTGCTGCTGCAAAAGCAATATCTATGCTGCAAT 882
786 TACCGCTCCGAGACGGATGATGACAGTCTATGAGCCATTTCAAGCCGATCATG 845
883 TTTCCATGTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 942
846 TCCAAAGTATGAGATGTTCCAGCTTACGCTGCTGCTGCTTACAGTGTGCTGACCTCC 905
943 TCAAGGTGATGAGATGATGATCACTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1002
906 CTATCTGAGGATCGGTTAGTGTCTTCAATCTATCTATCAAGGACCAAGCTGCTG 965
1003 TTTATCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1062
966 GAATTTGTCMAAGCTTTTAACTGCTATGATGATGATGATGATGATGATGATGATGAT 1025
1063 GAAGTTGTAATACTTTTAACTTACATGATGATGATGATGATGATGATGATGATGATG 1122
1026 CTTAACCTTCCCGGCTGCTGATGATGATGATGATGATGATGATGATGATGATGATG 1085
1123 CTTAAATGCTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1182
1086 AATGAGCTTCCATACATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1145
1183 AATGAGTCCAT 1242
1146 AGTCTTCCATATATGCTTAAACAGACAAAGATGATGATGATGATGATGATGATGATG 1205
1243 AGTCTTCCATATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1302
1206 CTGTTGAGAACCTTAAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1265
1303 TTTGTTGAAATTTTGGCATGTTTACCTCATGCACTGCTGCTGCTGCTGCTGCTGCTG 1362
1266 GAGAGCCATCTCTGAGAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1325
1363 GAGAGTCTGTTCTATTAAGATGATGATGATGATGATGATGATGATGATGATGATGAT 1422
1326 TCGATCTGCTCTGATCAAAAGATTTGCTGAGAGAGATTTCTCCATTTGGAAGAG 1385
1423 TCTATTCGACATCAAGACAGAGATGCTGTTGATGAGAAATTTCTCAATTTGAGAT 1482
1386 GAGGAGAGGGGGCGCAAGAACTTTTCAATTTCAAAAAAGCAAGAGAGTCAAAACA 1445
1483 GAAAGGAGAGAGAGTGAAGAAATGCTGATCATTAAGAAAGACAAAGAAAGCTAAG 1542
1446 GAGGATGAAAAAGAGAAAGCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1505
1543 ATTGAAGAGATTAAGAAAGAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1602
1506 AAGGAG 1551
1603 TCCAAAGACACAGTGTGTAAGAAACAGATTCAAAGAGAGAGAGAGAGAGAGAGAG 1648

RESULT 10
US-09-817-913-4

Sequence 4, Application US/09817913
Patent No. US20020061860A1
GENERAL INFORMATION:
APPLICANT: Li, Zuomei
APPLICANT: Bonifis, Claire
APPLICANT: Besteman, Jeffrey
TITLE OF INVENTION: Inhibition of Specific Histone Deacetylase Isoforms
FILE REFERENCE: 106101.145
CURRENT APPLICATION NUMBER: US/09/817,913
CURRENT FILING DATE: 2001-03-26
PRIOR APPLICATION NUMBER: US 60/192,157
PRIOR FILING DATE: 2000-03-24
NUMBER OF SEQ ID NOS: 33
SOFTWARE: PatentIn version 3.1
SEQ ID NO 4
LENGTH: 1985
TYPE: DNA
ORGANISM: Human
US-09-817-913-4

Query Match 49.4%; Score 795.6; DB 9; Length 1985;
Best Local Similarity 72.4%; Pred. No. 2,9e-234;
Matches 1032; Conservative 0; Mismatches 394; Indels 0; Gaps 0;

126 GGCACCCGAGAGAGTCTGTTACTACTACGACGGGATGTTGGAATTAATTATTAAGA 185
223 GGGCGCAAAAAAGTCTGTTACTACTACGACGGTGTATTTGAAATTAATTATTAAGA 282
186 CAAAGCCACCAATGAAGCTTACCGAATCCGATGATCTCATTAATTTGCTGCACTAT 245
283 CAGGGTCATCCCATGAAGCTCATAGAAATCCGATGACCCATTACTTGCTGTTAAATAT 342
246 GGTCTACCGAAAAAGAAATCTATCGCCCTACAAAGCCATGCTGAGGAATAGC 305
343 GGGTTACACAGAAAAAGAAATATATAGCCCATTAAGCCATGCTGAGGAATATCA 402
306 AAGTACCAAGCGATGATCATTAATTTCTTGCGCTCATCCGTCAGATTAATCATGTCG 365
403 AATATCACTGATGATGATATTAATTTCTACGCTCAATTAACAGATTAATCATGTC 462
366 GAGTACGACAGAGATGACAGATTCACGTTGAGAGATGAGATGATGATGATGATGATG 425
463 GAGTATAGTAAAGATGATGATTAATTTATGAGAGATGATGATGATGATGATGATGATG 522
426 CTGTTGAGTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 485
523 CTCTTTAGTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 582
486 AAGCAGAGAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 545
583 CGACACAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 642
546 GAGGATCTGCTTCTGTTACGATGATGATGATGATGATGATGATGATGATGATGATGATG 605
643 GAAACATCAGGATCTGTTACGATGATGATGATGATGATGATGATGATGATGATGATGATG 702
606 TATACACAGAGAGGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 665
703 TATCATAGAGAGCTTATATATGATGATGATGATGATGATGATGATGATGATGATGATGAT 762
666 GCCTTCAACACAGAGAGCGGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 725
763 GCTTTTATATACAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 822
726 CCAAGAACTGGGAGCTTACGAGATGATGATGATGATGATGATGATGATGATGATGATGATG 785
823 CTTGACACAGAGAGCTTACGAGATGATGATGATGATGATGATGATGATGATGATGATGATG 882
786 TACCCGCTCCAGAGAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 845
883 TTTTCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 942
846 TCACAAAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 905

943 TCAAGTATGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1002
906 CTATCTGGGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 965
1003 TATCTGGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1062
966 GAATTTGTCAGAGCTTAACTGATGATGATGATGATGATGATGATGATGATGATGATGATG 1025
1063 GAGGTTGTAAGAACTTTAACTTACATGATGATGATGATGATGATGATGATGATGATGATG 1122
1026 CTTACGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1085
1123 CTTAATGTTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1182
1086 AATGAGCTTCCATACATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1145
1183 AAGAGTTGCTCATATATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1242
1146 AGTCTTCCATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1205
1243 AGTCTTCCATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1302
1206 CTGTTGAGAACTTAAATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1265
1303 TTGTTGAAATTTTGGCATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1362
1266 GAGAGCCCATCCCTGAGAGATGATGATGATGATGATGATGATGATGATGATGATGATG 1325
1363 GAAAGTCTGTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1422
1326 TCGATCTGCTCTGACAAACGAATGCTGAGAGAGATGATGATGATGATGATGATGATG 1385
1423 TCTATTCAGATCATGACAAACGATGATGATGATGATGATGATGATGATGATGATGATG 1482
1483 GAAAG 1542
1446 GAGATGAAAG 1505
1543 ATTGAAGAGATGAG 1602
1506 AAGGAG 1551
1603 TCACAG 1648

RESULT 11
US-09-817-538-4
Sequence 4, Application US/09817538
Patent No. US20020137162A1
GENERAL INFORMATION:
APPLICANT: Li, Zuomei
APPLICANT: Bonifis, Claire
APPLICANT: Besteman, Jeffrey
TITLE OF INVENTION: Antisense Oligonucleotide Inhibition of Specific Histone
FILE REFERENCE: 106101.144
CURRENT APPLICATION NUMBER: US/09/817,538
CURRENT FILING DATE: 2001-03-26
PRIOR APPLICATION NUMBER: US 60/192,157
PRIOR FILING DATE: 2000-03-24
NUMBER OF SEQ ID NOS: 33
SOFTWARE: PatentIn version 3.1
SEQ ID NO 4
LENGTH: 1985
TYPE: DNA
ORGANISM: Human
US-09-817-538-4

Query Match 49.4%; Score 795.6; DB 10; Length 1985;
Best Local Similarity 72.4%; Pred. No. 2,9e-234;

| Matches 1032; Conservative 0; Mismatches 394; Indels 0; Gaps 0; | | | | |
|---|------|---------|--|------|
| QY | 126 | GGCACC | CGAGAAAGTCTGTACTACTACTACGACGGGAGATGTTGAATTAATCTTTATGA | 185 |
| DB | 223 | GGCGCA | AAAAAAGTCTGTCTCTCTACTACGACGGGATTTGGAATTTTATTTATGA | 282 |
| QY | 186 | CAAGCC | CAACCAATGAAGCTCTACCGAATCCGATGATCTATTAATTTGCTGCTCAAT | 245 |
| DB | 283 | CAGGGT | CATCCCTGAAAGCTCTATGAATCCGATGATCCATTAATTTGCTGTTAATTA | 342 |
| QY | 246 | GGCTCT | ACCGAAATATGAAATCTATCGCCCTCAAAAAGCCAAATGCTGAGGATGACC | 305 |
| DB | 343 | GGCTTA | CACAGAAAAATGAAAAATATAGCCCAATAAAGCCATCCGAGAAAAAGACA | 402 |
| QY | 306 | AAGTAC | CAACGAGATGATCAATTAATTTGCGCTCCATCCGTCAGATTAATCATGTG | 365 |
| DB | 403 | AATATC | ACAGATGATGATATCAATTAATTTCTACGGCTCAATTAAGACCAATTAACATGCT | 462 |
| QY | 366 | GAGTAC | AGAGAGAGATGACAGATTCAAAGTGTGAGAGACTGTCCAGTATTGATGAC | 425 |
| DB | 463 | GAGTAT | AGTATAGATGACATATATTTAATGTTGAGAAAGATTGTCCAGGTTTATGGA | 522 |
| QY | 426 | CTGTTG | AGTCTCTGATGTTGTCTACTGCTGCTTCTGTGCAAGTCTGTGAATTTAAT | 485 |
| DB | 523 | CTCTTG | AGTCTTGTGAGCTCTCACTGCGGCTTCAGTTGCTGAGCTGTGAAGTTAAAC | 582 |
| QY | 486 | AAGCAG | CAGCGGACATCCGCGTAATGCGGCTGGGGCTGTGACATGCAAAAGAGTCC | 545 |
| DB | 583 | CGACAA | CAGCTGATATGCTGTTAATGGCTGAGAGATTACATATGTAAGAAATAC | 642 |
| QY | 546 | GAGGCA | TCCTGCTTCTGTTACGTCATTAATGATGCTGTGGCCATCCCTGGAATCTAAAG | 605 |
| DB | 643 | GAGGAT | CAAGGATCGGATCGCTTACGTTAATGATATGCTGCTCCATCCCTGAATTAACAAAG | 702 |
| QY | 606 | TATCACA | AGAGGCTGCTGATCATGATGATTAATTCACATGCTGTAAGGCGCTGGAAGAG | 665 |
| DB | 703 | TATCAT | CAGAGATCTTAATATATGATATGATTAATTCATATGATGCTGTCGAAGAA | 762 |
| QY | 666 | GGCTTC | ACCAACGAGCGGCTGATGATGCTCTTTCATTAAGATGAGAGTCTTC | 725 |
| DB | 763 | GCTTTT | ATTAACAACATGCTGTAAGACGTAATCCATTAATTAATGAGAAATCTTT | 822 |
| QY | 726 | CCAGAA | CTGGGACCTACCGGAGTACCGGGCTGCAAAAGACAAGATTAATGCTGTTAAC | 785 |
| DB | 823 | CCGGCA | CAGGAGACTTGGAGGATATTTGCTGCTGAAAAAGCAAAATATGCTGCAAT | 882 |
| QY | 786 | TACCCG | CTCCGAGCGGATTTGATGACGATCTATGAGCCATTTTCAAGCCGCTATG | 845 |
| DB | 883 | TTTCCA | ATGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG | 942 |
| QY | 846 | TCCAAG | TATGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG | 905 |
| DB | 943 | TCAAA | GATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG | 1002 |
| QY | 906 | CTATCG | GGGAGTGGTGGTCTTCAATCTATCTATCAAAAGACACGCAAGTGTGTG | 965 |
| DB | 1003 | TATCTG | GTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG | 1062 |
| QY | 966 | GAAATT | GTCAAGAGCTTTAACTGCTATGCTGATGCTGGAGCGGTGTTACACATTT | 1025 |
| DB | 1063 | GAAAGT | GTAAAAAATTTTAACTTAACTTAACTTAACTTAACTTAACTTAACTTAACTT | 1122 |
| QY | 1026 | CGTAA | CGTGGTGGGCTGCTGATGATGATGATGATGATGATGATGATGATGATGATG | 1085 |
| DB | 1123 | CGTAA | CGTGGTGGGCTGCTGATGATGATGATGATGATGATGATGATGATGATGATG | 1182 |
| QY | 1086 | AATGAC | CTTCATACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG | 1145 |
| DB | 1183 | AAGGAT | GTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG | 1242 |
| QY | 1146 | AGTCTT | CCAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG | 1205 |
| DB | 1243 | AGTCTT | CCAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG | 1302 |

| | | | | |
|---|------|---------|---|------|
| QY | 1206 | CTGTTG | AGAACTTAAATGCTGCGACGACCTGGGGTCCAAACGAGGCGATTCCT | 1265 |
| DB | 1303 | TTGTTG | AAATTTTGGGATGATTAACCTATGACACCTGGGTGTCAGATGCAAGTATTTCA | 1362 |
| QY | 1266 | GAGAGC | GCATCCCTGAGGAGTGGCGGATGAGACGAAGACCACTTGAACAAGCCATC | 1325 |
| DB | 1363 | GAAATG | CTGTTCAAGAAACAGTGGAGATGAAAGATGAGAAAGATTCACAGAAATTT | 1422 |
| QY | 1326 | TGATCT | GCTCTGACAAAGAAATGCTGTGAGAAAGATTCGATTCGATTCGAAGAG | 1385 |
| DB | 1423 | TCTATT | CGATCAACAGACGAGAGTGTGATGAAAGATTTCTCAATTTCTGAGAT | 1482 |
| QY | 1386 | GAGGAG | AGGGGGCGCAAGAACTTTTCAACTTCAAAAAAGCCAAAGAGTCAAAACA | 1445 |
| DB | 1483 | GAAAGAG | AGAGAGTGAAGAAATGTGCTGATCATTAAGAAAGCAAAAGAAAGTATGA | 1542 |
| QY | 1446 | GAGATG | AAAAAGAAAGCCAGAGAGAAAGAAATACCGAAGAGAGAAACC | 1505 |
| DB | 1543 | ATTGAA | AGATTAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGTAA | 1602 |
| QY | 1506 | AAGGAG | AGAAAGCCAAAGGGTCAAGAGAGAGCCAAAT | 1551 |
| DB | 1603 | TCCAAG | ACACAGTGTGAAAAAACAGATACCAAGAAACCAAT | 1648 |
| RESULT 12 | | | | |
| US-09-796-692-5317 | | | | |
| ; Sequence 5317, Application US/09796692 | | | | |
| ; Publication No. US20020198362A1 | | | | |
| ; GENERAL INFORMATION: | | | | |
| ; APPLICANT: Gaiger, Alexander | | | | |
| ; APPLICANT: Algate, Paul A. | | | | |
| ; APPLICANT: Manion, Jane | | | | |
| ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DETECTION, DIAGNOSIS AND THERAPY | | | | |
| ; FILE REFERENCE: 2077.001200 | | | | |
| ; CURRENT APPLICATION NUMBER: US/09/796,692 | | | | |
| ; PRIOR APPLICATION NUMBER: 60/186,126 | | | | |
| ; PRIOR FILING DATE: 2000-03-01 | | | | |
| ; PRIOR APPLICATION NUMBER: 60/190,479 | | | | |
| ; PRIOR FILING DATE: 2000-03-17 | | | | |
| ; PRIOR APPLICATION NUMBER: 60/200,545 | | | | |
| ; PRIOR FILING DATE: 2000-04-27 | | | | |
| ; PRIOR APPLICATION NUMBER: 60/200,303 | | | | |
| ; PRIOR FILING DATE: 2000-04-28 | | | | |
| ; PRIOR APPLICATION NUMBER: 60/200,779 | | | | |
| ; PRIOR FILING DATE: 2000-04-28 | | | | |
| ; PRIOR APPLICATION NUMBER: 60/200,999 | | | | |
| ; PRIOR FILING DATE: 2000-05-01 | | | | |
| ; PRIOR APPLICATION NUMBER: 60/202,084 | | | | |
| ; PRIOR FILING DATE: 2000-05-04 | | | | |
| ; PRIOR APPLICATION NUMBER: 60/206,201 | | | | |
| ; PRIOR FILING DATE: 2000-05-22 | | | | |
| ; PRIOR APPLICATION NUMBER: 60/218,950 | | | | |
| ; PRIOR FILING DATE: 2000-07-14 | | | | |
| ; PRIOR APPLICATION NUMBER: 60/222,903 | | | | |
| ; PRIOR FILING DATE: 2000-08-03 | | | | |
| ; PRIOR APPLICATION NUMBER: 60/223,416 | | | | |
| ; PRIOR FILING DATE: 2000-08-04 | | | | |
| ; PRIOR APPLICATION NUMBER: 60/223,378 | | | | |
| ; PRIOR FILING DATE: 2000-08-07 | | | | |
| ; NUMBER OF SEQ ID NOS: 9597 | | | | |
| ; SOFTWARE: FastSeq for Windows Version 3.0 | | | | |
| ; SEQ ID NO 5317 | | | | |
| ; LENGTH: 546 | | | | |
| ; TYPE: DNA | | | | |
| ; ORGANISM: Homo sapiens | | | | |
| US-09-796-692-5317 | | | | |
| Query Match 33.4%; Score 538; DB 10; Length 546; | | | | |
| Best Local Similarity 99.1%; Pred. No. 4,2e-155; | | | | |


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? FILE REFERENCE: 5718-44,
? CURRENT APPLICATION NUMBER: US/09/883,720
? CURRENT FILING DATE: 2001-06-18
? PRIOR APPLICATION NUMBER: 09/282,305
? PRIOR FILING DATE: 1999-03-31
? NUMBER OF SEQ ID NOS: 18
? SOFTWARE: PatentIn Ver. 2.0
? SEQ ID NO 7
? LENGTH: 1943
? TYPE: DNA
? ORGANISM: Zea mays
? FEATURE:
? NAME/KEY: CDS
? LOCATION: (57)..(1610)
? US-09-883-720-7

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|-----------------------|----------------|--------------------|----------|-------------|
| Query March | 31.2% | Score 502.6 | DB 9 | Length 1943 |
| Best Local Similarity | 65.5% | Pred. No. 6.9e-144 | | |
| Matches 768 | Conservative 0 | Mismatches 399 | Indels 6 | Gaps 2 |

| | | | |
|----|-----|---|-----|
| QY | 134 | GAGGAAGTCTGTTACTACTACATCAAGAGGGGAGTGTGAAATTACTATTTATGACCAAGGCCA | 193 |
| Db | 122 | GGCGCGGTGTGCTACTTCTACAGACCGGGAATGAGGCACTACACTACAGGACAGGCCA | 181 |
| QY | 194 | CCCAATGAAGCCTCAACCGAATCCGCATGACTCATTAATTTGCTGCTCAACTATAGTCTCTA | 253 |
| Db | 182 | TCCGATGAAGCGCACCGCATCCGGATAGCGCACTGGTGGTGGGCGCTTACGGCTCCT | 241 |
| QY | 254 | CCGAAAAATGGAATCTATGCGCCTCACAAAGCCAAATGCTGAGAGATGACCAATACCA | 313 |
| Db | 242 | CAACAGATGAGGGTGTACCGCCCAACCCGGCCGCGACACCGGACCTTCGCGCTTCCA | 301 |
| QY | 314 | CAGCGATGACTACATTAATTTCTTGCGCTCCATCCGTCAGATTAATGTGAGAGTACAG | 373 |
| Db | 302 | CGCGGACACTACATCAACTTCTCTGCTCCGTACACGCGGAAAGCAGCAGAACCAAGT | 361 |
| QY | 374 | CAACAGATGACAGATTCAACTTTGATGAGGACTGTCCAGTATTCGATGAGCTTTTGA | 433 |
| Db | 362 | CCGCTGCTCAAGCGCTTCAACGTCGGGAGGACTGCCCGCTTCGACGGGCTCTACAG | 421 |
| QY | 434 | GTTCTGTCAATTGTCTACTGTGTGTTCTGTGTGCAAGTGTGTGAACTTAATACAGCA | 493 |
| Db | 422 | CTTCTGCAGACTATGCGGCGCTCCGTGCGCGGCGCTCAAGCTCAACACAGGCCA | 481 |
| QY | 494 | GACGACATCCCGTGAATTTGGGCTGGGGGCTTCGACCATGTGAAAGAAAGTCCGAGGATC | 553 |
| Db | 482 | ---TGACATCCCATCACTGCTCGGGGGGCTTGACACACGCAAGAAAGTGGAGGCGTC | 538 |
| QY | 554 | TGGCTTCTGTACGTCAAATGATATGCTTGGCCATCTCGAAGTCTAAAGTATACCA | 613 |
| Db | 539 | GGGCTTCTGTACGTCAAATGATATGCTGTGCTGSCATATCGAGCTGCTCAACATACGA | 598 |
| QY | 614 | GAGGTGCTGTACATTGACATTGATATTCAACATGTGACGCGGTGGAAGAGGCTTCTA | 673 |
| Db | 599 | GAGAGTTCTGTATGTCGATATCGAATATCCACCATGATGATGAGTGGAGAGGCTTCTA | 658 |
| QY | 674 | CACACCGGACCGGGTCATGACTGTGTCTCTTATTAAGTATGGAGATTTCCACGAAGC | 733 |
| Db | 659 | CACACAGATAGGGTTATGACTGTCTCGTTCCACAAGTTTGGTATTAATTTCCAGAGAAC | 718 |
| QY | 734 | TGGGGAACCTACGGGATACCGGGGCTGGCAAGACAAAGTATTAATGTGTATTACTACCGCT | 793 |
| Db | 719 | AGGGGATATCCGTGACATTTGGGCACTCAAAAGGAAGTACTATCCCTGAAATGTCCCTCT | 778 |
| QY | 794 | CCGAGACGGGATTAATGACGAGTCTTAATGAGGCCATTTCAAGCGGCTATGTCCAAAGT | 853 |
| Db | 779 | AGATGATGGGATTAATGATGAAGGTACCAAGTCCCTTTTAAAGCCAAATATGAGGCAAAAT | 838 |
| QY | 854 | AATGAGATGTTCCAGCTTAGTGCAGTGGTCTTAAGTGTGGCTCAGACTCCCTATCTGG | 913 |
| Db | 839 | TATGAGGATTTTCCGCGCTGTGTGCAAGTTGTCTTAATGTGTGCTGATTCCTTGTCTGG | 898 |
| QY | 914 | GGATCGTATAGGTTGCTTCAATCTATCTATCAAGGACACGCGCAAGTGTGTGGAATTGT | 973 |

| | | | |
|----|------|--|------|
| Db | 899 | GGATAGGTTGGCGCTCTTCAACCTCTCAATCCAAAGCTCATGCGGAATGTGTAGATATAT | 958 |
| Qy | 974 | CAAGAGCTTTAACCTGCGCTATGCTGATGCTGGAGCGGTGTTACCAATTCGTAACGT | 1033 |
| Db | 959 | GAGGTCCTTTCAAGCTTCCATTGTTGGCTCTTGGTGGTGGATATATCAATTAAGAAATGT | 1018 |
| Qy | 1034 | TGCGCGGTGCTGCACATATAGACACAGCTGTGGCCCTTGGAATCGAGATCCCTTAATGAGCT | 1093 |
| Db | 1019 | TGCAGCGCTGTTGGTGTATGAGACTGGAGTTGCTCTTGCCCAAGAGCCTGAAGCAAGAT | 1078 |
| Qy | 1094 | TCCATACATGACTACTCTTTGAATCTTTGGACCGAGATTTCAAGCTCCACATCAAGTCTTC | 1153 |
| Db | 1079 | GCCGTGTAATGAGACTATGAAATCTTCGGGTCCAGATTTACACTCTTATGTTGGACCAAG | 1138 |
| Qy | 1154 | CAATATGACTAACCGAACAACGATGATCTGAGAAATCAAACGCACTGTTTGA | 1213 |
| Db | 1139 | TAACTGAGAGAACAAATATACACGACAACACTGGATGATATATGACTTAAACTTCGGA | 1198 |
| Qy | 1214 | GAACCTTAGAATGCTGGCGCAGCGACCTGGGGTCCAAACGACGCGA---TTCCTAGGA | 1270 |
| Db | 1199 | TAACTTTTCAAAACTTGGACATGCTCTTAAGTGTCACTTTTCAGAGAGAGTTCCTGACAC | 1258 |
| Qy | 1271 | CGCATCCCTGAGAGAGTGGCCATGAGACGA | 1303 |
| Db | 1259 | AGAAATACCTGAGCAAGTGAAGTCAAGATGA | 1291 |

RESULT 15
US-09-883-720-5
; Sequence 5, Application US/09883720
; Patent No. US20020022256A1
GENERAL INFORMATION

; GENERAL INFORMATION:
 ; APPLICANT: Baldwin, Donald A.
 ; APPLICANT: Briggs, Steven P.
 ; APPLICANT: Crane, Virginia C.
 ; TITLE OF INVENTION: Maltize Histone Deacetylases And Their Uses
 ; FILE REFERENCE: 5718-44,
 ; CUMULATIVE AND/OR OTHER NUMBERS: 15/00/003 720

| | | | | |
|-----------------------|-------|--------------------|----------|-------------|
| Query Match | 31.1% | Score 501.8 | DB 9 | Length 2019 |
| Best Local Similarity | 65.3% | Pred. NO. 1.2e-143 | | |
| Matches 753 | 0 | Mismatches 397 | Indels 3 | Gaps 1 |

| | | | | | | | | | | | | |
|----|-----|-------------|------------|---------|----------|------------|---------|----------|---------|--------|--------|-----|
| OY | 121 | TCGAGGGCACC | CGGAGGAAA | AGTCTGT | TACTACT | CTACGACGG | GGAGATG | TGGAAAT | TACTACT | 180 | | |
| Db | 189 | CGGACGGG | TCGACGCGCG | CGCTCTG | TACTACT | CTTACGACGG | AGATGGG | CAACTACT | | 248 | | |
| OY | 181 | ATGACAA | GAGGCAC | CCCATG | GAAGCTCA | CCGAAAT | CCGATAC | TCAAT | ATTTGG | CTCTCA | 240 | |
| Db | 249 | ACGGGCA | GGGCGAC | CCCGAT | GAGCCG | CATTCG | CATATAC | CCACG | CGCTG | CTCGGC | 308 | |
| OY | 241 | ACTATG | TCTCTAC | CGAAAAT | GTATG | CGCCCT | CAACAA | GCCCAT | GTGAG | GAGA | 300 | |
| Db | 309 | GCTAG | GGCTCT | CTTGAC | CAATG | GAAGT | GTTCG | CGCCCT | CAAC | CTGCGG | ACCGG | 368 |
| OY | 301 | TGACCA | AGTAC | CACAG | CGAT | ACTAC | TAAAT | TTTGC | CGCTCC | ATTCG | AGAT | 360 |
| Db | 369 | TCCTCC | GGCTT | CCACG | CGCAT | TAGCT | CTCTT | CTCCGG | TCTG | TACAC | CCCGAA | 428 |

QY 361 TGTGAGTACAGCAGATGACAGATTCAAGTTGTGAGAGACTGTCCAGTATTCG 420
DB 429 AGCAGGACAGATCCGGCGCTCAAGCGCTTCAAGCTGCGGAGAGACTGCCCGCTTCG 488
QY 421 ATGGCTGTGTTGAGTTCTGTCAAGTTGTCTACGTGTGTTCTGTGCAAGTGTGAAAC 480
DB 489 ACGGCTCTACAGTTCTGTGACAGTACGCGGGGGCTGTGTGGCGGCCGCTCAAGC 548
QY 481 TTAAATAGCAGCAGACCGACATCGCCCGTGAATTGGGCTGGGGGCTGCACCATCAAGA 540
DB 549 TCAACCAATGGCCA--TGATATGCCCATCAACTGAGCGGCACTCCACCGCAAGA 605
QY 541 AGTCGAGGACATCTGCTTCTGTACGTCATGATGATATGTCCTTGCCATCTGGAATGC 600
DB 606 AGTCGAGGCTCTCGGGTTTGTATGATGATGATGATGATGATGATGATGATGATGATG 665
QY 601 TAAAGTATCACCAAGGAGGCTGTACATGATGATGATGATGATGATGATGATGATGATG 660
DB 666 TCAAGTACACACGCGCTTCTGTACGTGACATGATGATGATGATGATGATGATGATGATG 725
QY 661 AAGAGGCTTCTACACCGGACCGGCTGATGATGATGATGATGATGATGATGATGATGATG 720
DB 726 AGGAGGCTTTTATATACACAGACCGGCTGATGATGATGATGATGATGATGATGATGATG 785
QY 721 ACTTCCAGGACATGAGGACCTACGAGATACCGGGCTGCGCAAGACAGATATGATGCTG 780
DB 786 ATTTCCCTGGGACAGGGGACATGATGATGATGATGATGATGATGATGATGATGATGATG 845
QY 781 TTAACCTACCGCTCCGAGCGGATGATGATGATGATGATGATGATGATGATGATGATGATG 840
DB 846 TGAATGTTCCCTGGAGCATGATGATGATGATGATGATGATGATGATGATGATGATGATG 905
QY 841 TCATGTCGAAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 900
DB 906 TAAATGGGCAAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 965
QY 901 ACTCCATATCTGGGAGATCGATTAGTGTCTCAATCTATCTATCAAGACACGCCAAGT 960
DB 966 ATTATATGTGCGGAGACAGTTGGCTGTTCACCTGTGATGATGATGATGATGATGATGATG 1025
QY 961 GTGTGAATTTGTCAAGACTTTAACTGCTATGCTGATGATGATGATGATGATGATGATGATG 1020
DB 1026 GTGTGAATTTATAGGCTCTTCAACGTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGAT 1085
QY 1021 CCATTCGTAAGTGTGCGCGGTGCTGACATATGAGACAGCTGCGCCCTGATACGAGA 1080
DB 1086 CCATTAAGAAAGTGTGACAGGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1145
QY 1081 TCCCTAATGAGCTTCCATACATGACTACTTTGAATCTTTGACACAGATTTCAAGCTCC 1140
DB 1146 TCACTGACAAAGATGCGACCTATGATGATGATGATGATGATGATGATGATGATGATGATG 1205
QY 1141 ACATGAGTCTTCCATATGACTTAACCAAGACAGATGATGATGATGATGATGATGATGATG 1200
DB 1206 ATGTGCTCCCAAGTACATGAGATATAAAACACACGCGCATCAATGATGATGATGATGAT 1265
QY 1201 AGGAGTGTGAGAACCTTGAATGCTGCGGCAAGCACTGGGGTCCAAACGAGGCGA 1260
DB 1266 CAAATCTTAGATATCTTCAAAATCCGACATGCTCTAGTGTCAAGTTCAAGAGC 1325
QY 1261 TTCTGAGAGCGC 1273
DB 1326 GACCTCCTGAGGC 1338

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